

Result No.	Score	Query Match	Length	DB	ID	Description
1	715	99.7	717	6	AR231454	AR231454 Sequence
2	715	99.7	1176	6	AR231456	AR231456 Sequence
3	593.4	82.8	717	6	AR482235	AR482235 Sequence
4	590.4	82.3	723	10	AF035617	AF035617 Mus musc
5	580.4	80.9	735	12	AF162270	AF162270 Synthet
6	574.2	80.1	735	12	AY725471	AY725471 Synthet
7	568.4	79.3	927	6	AX111695	AX111695 Sequence
8	555.8	77.5	716	6	AX839011	AX839011 Sequence
9	550.2	76.7	723	12	AY374128	AY374128 Synthet
10	547.6	76.4	807	6	BD234870	BD234870 Continuo
11	547.6	76.4	807	6	AR311194	AR311194 Sequence
12	546	76.2	1815	12	AF189283	AF189283 Synthet
13	541.4	75.5	725	6	A97142	A97142 Sequence
14	539.2	75.2	811	6	CQ768808	CQ768808 Sequence
15	539.2	74.7	811	6	CQ802042	CQ802042 Sequence
16	535.8	74.7	750	12	AF042255	AF042255 Synthet
17	535.6	74.7	990	6	AX111696	AX111696 Sequence
18	534.2	74.5	771	6	AR407830	AR407830 Sequence
19	534.2	74.5	780	6	AR407831	AR407831 Sequence

20	531	74.1	717	12	AF367377	AF367377 Synthetic
21	524.8	72.2	789	12	AF468378	AF468378 Mus muscu
22	523.8	73.1	894	6	AR316970	AR316970 Sequence
23	522.2	72.8	726	6	A46598	A46598 Sequence 25
24	521.6	72.7	726	6	A46594	A46594 Sequence 29
25	521.6	72.7	726	6	AR063195	AR063195 Sequence
26	520.4	72.6	732	6	E13410	E13410 cDNA encodi
27	517.8	72.2	2364	6	E13412	E13412 cDNA encodi
28	517.4	72.2	1797	6	I84705	I84705 Sequence 2
29	516.6	72.1	738	12	AF635846	AF635846 Synthetic
30	515.8	71.9	719	6	AR100151	AR100151 Sequence
31	515.8	71.9	720	6	AR117135	AR117135 Sequence
32	513.4	71.6	61582	2	RN499920	AL603720 RatIus no
33	513.4	71.6	61804	2	AC027647	Continuation (4 of
34	513.4	71.6	110000	2	AC074223	Continuation (4 of
35	513.4	71.6	138860	2	AC055703	AC055703 Mus muscu
36	512.4	71.6	276248	2	AC087561	AC087561 Mus muscu
37	512.6	71.5	726	6	A46596	A46596 Sequence 27
38	512.6	71.5	726	6	AR063196	AR063196 Sequence
39	512.4	71.5	723	12	AY307993	AY307993 Synthetic
40	512	71.4	810	6	CQ873224	CQ873224 Sequence
41	512	71.4	810	6	CQ876881	CQ876881 Sequence
42	511.8	71.4	717	10	AF055535	AF055535 Mus muscu
43	511.8	71.4	786	12	AF279665	AF279665 Synthetic
44	511.8	71.4	2213	2	AC087118	AC087118 Mus muscu
45	510.8	71.2	729	12	AY171038	AY171038 Synthetic

ALIGNMENTS

RESULT 1
AR231454

DEFINITION Sequence 1 from patent US 6451995.

VERSION AR231454.1 GI:27272556

SOURCE Unknown.

Unclassified.

AUTHORS Cheung, N.-K.V., Larson, S.M., Guo, H.-F., Rivlin, K. and Sadelain, M.

anti-ganglioside GD2 antibodies, cells expressing same and related

JOURNAL Patent: US 6451995-A 1 17-SEP-2002;

source	1. .717
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/mol_type="genomic DNA"

ORIGIN

Query Match	99.7%	Score 715;	DB 6;	Length 717;
Test result 100.0%	100.0%	Score 715;	DB 6;	Length 717;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGTGAACCTGCAGCAGTCAGGACCTGAACCTGGTGNAGCCCTGGGGCTTCAGTGAAGATA 60

Db 1 CAGGTGAACCTGCAGCAGTCAGGACCTGAACCTGTGNAGCCCTGGGGCTTCAGTGAAGATA 60

61 TCCTGCAGACTTCTGGANACAAATTCACCTGATACACCATGCACCTGGGTGAAGCAGAGC 12

Db 61 TCCTGCAGACTTCTGGANACAAATTCACCTGATACACCATGCACCTGGGTGAAGCAGAGC 12

121 CATGGAAGAGCCCTTGAGTGGATTGGAGCTATTATCCTAACAAATGGTACTACTAC 18

Db 121 CATGGAAGAGCCCTTGAGTGGATTGAGGTAATTATCCTAACAAATGGTGTACTACTAC 18

181 AAGCAGAGTTCAGGCCAGGCCACATTGACTGTAGACAAAGTCTCCAGCACAGCCTAC 24

Db 181 AAGCAGAAGTTC AAGGCAAGGCCACATTGACTGTAGACAAGTCTCCAGCACAGCCTAC 24

QY 241 ATGAGAGCTCCGACAGCTGACATCTGAGGATTCTGCACTATTACTGTGCAAGAGATACT 300
DB 241 ATGAGAGCTCCGACAGCTGACATCTGAGGATTCTGCACTATTACTGTGCAAGAGATACT 300
QY 301 ACGGTCCCGTTTGCTTACTGAGTCCAAAGGACACAGGTCAACCTGCTCTCCAGGTGAGGC 360
DB 301 ACGGTCCCGTTTGCTTACTGAGTCCAAAGGACACAGGTCAACCTGCTCTCCAGGTGAGGC 360
QY 361 GGTTCAGGCGGAGGTGGCTCTGGGCGGATCGGACATCGAGCTCACTCACTCCCA 420
DB 361 GGTTCAGGCGGAGGTGGCTCTGGGCGGATCGGACATCGAGCTCACTCACTCCCA 420
QY 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCACTACCTGTCAGTGCAGCTCAAGT 480
DB 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCACTACCTGTCAGTGCAGCTCAAGT 480
QY 481 ATAGTTACATGACCTGTATCCAGACAGAGAGCTGTCACTCTCCCAAAAGATGATTTAT 540
DB 481 ATAGTTACATGACCTGTATCCAGACAGAGAGCTGTCACTCTCCCAAAAGATGATTTAT 540
QY 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGTCAGTGCAGTGGTGGACC 600
DB 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGTCAGTGCAGTGGTGGACC 600
QY 601 TCTTATTTCTCTCACATCAGCAGCAGTGAAGCTGTAGATGCTGCACCTTATTACTGTCAT 660
DB 601 TCTTATTTCTCTCACATCAGCAGCAGTGAAGCTGTAGATGCTGCACCTTATTACTGTCAT 660
QY 661 CAGCGAGATGATTACCCGCTCAGCTTGGTGTCTGGACACAGTTGGAATTAACCG 717
DB 661 CAGCGAGATGATTACCCGCTCAGCTTGGTGTCTGGACACAGTTGGAATTAACCG 717

RESULT 2
AR231456
LOCUS AR231456 1176 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6451995.
ACCESSION AR231456
VERSION AR231456.1 GI:27272558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Cheung,N.-K.V., Larsen,S.M., Guo,H.-F., Rivlin,K. and Sadetain,M.
TITLE Single chain Fv polynucleotide or peptide constructs of anti-ganglioside GD2 antibodies, cells expressing same and related methods
JOURNAL Patent: US 6451995-A 3 17-SEP-2002;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 99.7%; Score 715; DB 6; Length 1176;
Best Local Similarity 100.0%; Pred.No.4,1e-211;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGAACTGCAGCAGTCAAGCTGAACTGGTGNAGCTGGGCTTCAGTGAAGATA 60
DB 1 CAGGTGAACTGCAGCAGTCAAGCTGAACTGGTGNAGCTGGGCTTCAGTGAAGATA 60
QY 61 TCTTCGCAAGACTCTGAGANCAAAATTCACTGAATATACCATGACCTGGGTGAAGCAGAC 120
DB 61 TCTTCGCAAGACTCTGAGANCAAAATTCACTGAATATACCATGACCTGGGTGAAGCAGAC 120
QY 121 CATGAAAGAGCCTTGAAGTGAATTGAGATTATCTTAACAATGCTGTAATACTTAC 180
DB 121 CATGAAAGAGCCTTGAAGTGAATTGAGATTATCTTAACAATGCTGTAATACTTAC 180
QY 181 AAGCAGAAATTCAAGGCGAAGCCACATTGATCTGTAGACAAGTCTTCAGACACGCTAC 240
DB 181 AAGCAGAAATTCAAGGCGAAGCCACATTGATCTGTAGACAAGTCTTCAGACACGCTAC 240

DB 181 AAGCAGAAATTCAAGGCGAAGCCACATTGATCTGTAGACAAGTCTTCAGACACGCTAC 240
QY 241 ATGAGAGCTCCGACAGCTGACATCTGAGGATTCTGCACTATTACTGTGCAAGAGATACT 300
DB 241 ATGAGAGCTCCGACAGCTGACATCTGAGGATTCTGCACTATTACTGTGCAAGAGATACT 300
QY 301 ACGGTCCCGTTTGCTTACTGAGTCCAAAGGACACAGGTCAACCTGCTCTCCAGGTGAGGC 360
DB 301 ACGGTCCCGTTTGCTTACTGAGTCCAAAGGACACAGGTCAACCTGCTCTCCAGGTGAGGC 360
QY 361 GGTTCAGGCGGAGGTGGCTCTGGGCGGATCGGACATCGAGCTCACTCACTCCCA 420
DB 361 GGTTCAGGCGGAGGTGGCTCTGGGCGGATCGGACATCGAGCTCACTCACTCCCA 420
QY 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCACTACCTGTCAGTGCAGCTCAAGT 480
DB 421 GCAATCATGTCTGCATCTCCAGGGAGAGAGTCACTACCTGTCAGTGCAGCTCAAGT 480
QY 481 ATAGTTACATGACCTGTATCCAGACAGAGAGCTGTCACTCTCCCAAAAGATGATTTAT 540
DB 481 ATAGTTACATGACCTGTATCCAGACAGAGAGCTGTCACTCTCCCAAAAGATGATTTAT 540
QY 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGTCAGTGCAGTGGTGGACC 600
DB 541 GACACATCCAAACTGGCTTCTGAGTCCCTGCTGCTTCACTGTCAGTGCAGTGGTGGACC 600
QY 601 TCTTATTTCTCTCACATCAGCAGCAGTGAAGCTGTAGATGCTGCACCTTATTACTGTCAT 660
DB 601 TCTTATTTCTCTCACATCAGCAGCAGTGAAGCTGTAGATGCTGCACCTTATTACTGTCAT 660
QY 661 CAGCGAGATGATTACCCGCTCAGCTTGGTGTCTGGACACAGTTGGAATTAACCG 717
DB 661 CAGCGAGATGATTACCCGCTCAGCTTGGTGTCTGGACACAGTTGGAATTAACCG 717

RESULT 3
AR482235
LOCUS AR482235 717 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 5 from patent US 6703015.
ACCESSION AR482235
VERSION AR482235.1 GI:47244217
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 717)
AUTHORS Solomon,B. and Frenkel,D.
TITLE Filamentous bacteriophage displaying an .beta.-amyloid epitope
JOURNAL Patent: US 6703015-A 5 09-MAR-2004;
FEATURES
source location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 82.8%; Score 593.4; DB 6; Length 717;
Best Local Similarity 90.1%; Pred.No.3,2e-173;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY 1 CAGGTGAACTGCAGCAGTCAAGCCTGAACTGGTGNAGCTGGGCTTCAGTGAAGATA 60
DB 1 CAGGTGAACTGCAGCAGTCAAGGCGCTGAGCTGGTGAAGCTGGGCTTCAGTGAAGATA 60
QY 61 TCTTCGCAAGACTCTGAGANCAAAATTCACTGAATATACCATGACCTGGGTGAAGCAGAC 120
DB 61 TCTTCGCAAGACTCTGAGANCAAAATTCACTGAATATACCATGACCTGGGTGAAGCAGAC 120
QY 121 CATGAAAGAGCCTTGAAGTGAATTGAGATTATCTTAACAATGCTGTAATACTTAC 180
DB 121 CATGAAAGAGCCTTGAAGTGAATTGAGATTATCTTAACAATGCTGTAATACTTAC 180
QY 181 AAGCAGAAATTCAAGGCGAAGCCACATTGATCTGTAGACAAGTCTTCAGACACGCTAC 240
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RESULT 5	AF162710	735 bp	mRNA	linear	SYN 13-JUL-2000
LOCUS	AF162710				
DEFINITION	Synthetic construct	single chain antibody	3C45 mRNA	partial cds.	
ACCESSION	AF162710				
VERSION	AF162710.1	GI:9081896			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 735)				
	Terrada, E., Kerchbaumer, R. J., Giunta, G., Galeffi, P., Himmeler, G. and Cambra, M.				

TITLE Fully 'recombinant ELISAs' for routine detection of Citrus tristeza closterovirus (CTV) in plant material

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 735)

AUTHORS Terada,B., Kerschbaumer,R.U., Himmler,G. and Cambra,M.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-1999) Plant Protection and Biotechnology, Instituto Valenciano de Investigaciones Agrarias, Carrtera Moncada-Naquera km. 4.5, Moncada, Valencia 46113, Spain

FEATURES

source

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/organism="synthetic construct"

/mol_type="rRNA"

/db_xref="taxon:32630"

/note="derived from variable regions of heavy and light chains of an antibody isolated from hybridoma cells of Mus musculus (BALB/c strain)"

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/protein_id="AA82631.1"

/db_xref="GI:9081897"

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ORIGIN

Query Match 80.9%; Score 580.4; DB 12; Length 735;

Best Local Similarity 88.8%; Pred. No. 3,7e-169;

Matches 639; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 1 CAGGTGAAGTCGACGAGTCAGACCTGAACTGCTGTGAGCGCTTCACTGAAGATA 60

DB 7 CAGGTGAAGTCGACGAGTCAGACCTGAACTGCTGTGAGCGCTTCACTGAAGATA 66

QY 61 TCCTGCAAGCTCTCTGAGAACAAATTCACGTAATACCCCTGAGCTGGGAGCAGAGC 120

DB 67 TCCTGCAAGCTCTCTGAGAACAAATTCACGTAATACCCCTGAGCTGGGAGCAGAGC 126

QY 121 CATGGAAGAGCCTTGAAGTGAATGAGGATTAATCTTAACATGGTGGTACTAATCT 180

DB 127 CATGGAAGAGCCTTGAAGTGAATGAGGATTAATCTTAACATGGTGGTACTAATCT 186

QY 181 AAGCAAGATTCAAGGCGAAGGCCAATTGACTGTAGACAACTCTCCAGCAGACCTAC 240

DB 187 AAGCAAGATTCAAGGCGAAGGCCAATTGACTGTAGACAACTCTCCAGCAGACCTAC 246

QY 241 ATGAGAGCTCCGAGCCTGACATCTGAGGATTCGAGCTGATTAATCTGCAAG--AGAT 297

DB 247 ATGAGAGCTCCGAGCCTGACATCTGAGGATTCGAGCTGATTAATCTGCAAGCCTTAT 306

QY 298 ACTACGGTCCCGTTTGTCTTACGTGGTCAAGGGACCAAGCTCAACCTCTCTCAGGTGA 357

DB 307 GATCACAATCACTTTGACTACTGGGGCAAGGACCAAGCTCAACCTCTCTCAGGTGA 366

QY 358 GGGGTTTCAGGGGAGGTGGCTCTGGCGGTGGCGGATTCGACATCGAGCTCACTAGTCT 417

DB 367 GGGGTTTCAGGGGAGGTGGCTCTGGCGGTGGCGGATTCGACATCGAGCTCACTAGTCT 426

QY 418 CCAGCAATCATGCTCTGAGGAGGAGAAAGGTACCAATGACCTGCGAGTGGCACTCA 477

DB 427 CCAGCAATCATGCTCTGAGGAGGAGAAAGGTACCAATGACCTGCGAGTGGCACTCA 486

QY 478 AGTAAAGTTTACATGACTGTGTACAGCAGAAAGCTGTCACTCCCCAAAAGATGATT 537

DB 487 AGTAAAGTTTACATGACTGTGTACAGCAGAAAGCTGTCACTCCCCAAAAGATGATT 546

QY 538 TATGACAATCCAAACTGGCTTCTGAGATCCCTGCTCGCTTCAGTGGCAGTGGGTCTGG 597

DB 547 TATGACAATCCAAACTGGCTTCTGAGATCCCTGAGACGCTTCAGTGGCAGTGGGTCTGG 606

QY 598 ACCTCTTATCTCTCATCAATCAGACGAGGCTGTAGATGCTGCCATTATTAATCTGC 657

DB 607 ACCTCTTATCTCTCATCAATCAGACGAGGCTGTAGATGCTGCCATTATTAATCTGC 666

QY 658 CATCAGCAGAGTATGATACCGGCTCAGCTTCGCTGTGGACACAGTTGGAATAAAGCG 717

DB 667 CACAGCTGAGATGATACCGGCTCAGCTTCGCTGTGGACACAGTTGGAATAAAGCG 726

RESULT 6

AY725471 735 bp DNA linear SYN 07-SEP-2004

LOCUS AY725471

DEFINITION Synthetic construct anti-alpha toxin ScFv-1A8 antibody gene,

complete cds.

ACCESSION AY725471

VERSION AY725471.1 GI:51859985

KEYWORDS

SOURCE

ORGANISM

synthetic construct

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 735)

AUTHORS Zhao,B. and Xu,C.

TITLE Cloning and sequencing of the scFv-1A8 gene anti-alpha toxin of clostridium perfringens type A

JOURNAL Chin. J. Prev. Vet. Med. 22, 30-33 (2000)

REFERENCE 2 (bases 1 to 735)

AUTHORS Zhao,B. and Xu,C.

TITLE Direct Submission

JOURNAL Submitted (06-AUG-2004) College of Life Science, Hebei Normal University, Yuhua Road, Shijiazhuang, Hebei 050016, China

FEATURES

source

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/cell_line="hybridoma 1A8"

/note="derived from Clostridium perfringens type A"

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/protein_id="AAU11282.1"

/db_xref="GI:51859985"

/translation="MQVTKQESGPDLYKPGALVTKISCKASGYFTSYDINMYKQRPQ GLEWIGWITPDGSTRKNEKFKKALITLADSSSTAYMQLSLTSENNAVYVCARYR YFYFDYWGQGTIVTVSSGGSGGSGGSDNVLITQSPALMSAPGERVMTCSASS SVSYHWYVQOKRGTSPKMYLTITSLMASGVPERVSGSGTSYSTLTISMEADATY YCQRSSYPTFGSGTKLEIKRAAE"

ORIGIN

Query Match 80.1%; Score 574.2; DB 12; Length 735;

Best Local Similarity 87.4%; Pred. No. 3,1e-167;

Matches 627; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 CAGGTGAAGTCGACGAGTCAGACCTGAACTGCTGTGAGCGCTTCACTGAAGATA 60

DB 4 CAGGTGAAGTCGACGAGTCAGACCTGAACTGCTGTGAGCGCTTCACTGAAGATA 63

QY 61 TCCTGCAAGCTCTCTGAGAACAAATTCACGTAATACCCCTGAGCTGGGAGCAGAGC 120

DB 64 TCCTGCAAGCTCTCTGAGAACAAATTCACGTAATACCCCTGAGCTGGGAGCAGAGC 123

QY 121 CATGGAAGAGCCTTGAAGTGAATGAGGATTAATCTTAACATGGTGGTACTAATCT 180

DB 124 CATGGAAGAGCCTTGAAGTGAATGAGGATTAATCTTAACATGGTGGTACTAATCT 183

QY 181 AAGCAAGATTCAAGGCGAAGGCCAATTGACTGTAGACAACTCTCCAGCAGACCTAC 240

DB 184 AAGCAAGATTCAAGGCGAAGGCCAATTGACTGTAGACAACTCTCCAGCAGACCTAC 243

QY 241 ATGAGAGCTCCGAGCCTGACATCTGAGGATTCGAGCTGATTAATCTGCAAGAGTACT 300

Db	244	ATGCAGCTCAGCAGCGCTGACTTCTTGAGAACTCTGCAGTCTAATTTCTGTGCAAGATACTA	303
Oy	301	ACGATCCCGTTGTCTTACTAGGGTCCAGGGAGCACAAGGTACCGGTCTCTCAGGTGGAGGC	360
Db	304	AGGTACTACTTTGACTACTCTAGGGGCCAAGGGACACAGGTACACCGTCTCTTCAGGTGAGGC	363
Oy	361	GGTTTCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGGACATCGAGTCACTCAGTCTCCA	420
Db	364	GGTTTCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGGACATGTGTCTACCCAGTCTCCA	423
Oy	421	GCAATCATGTCTGCATCTTCAGGGGAGAAAGTTCACCATGACCTGCAGTGGCAGCTTCAAGT	480
Db	424	GCAATCATGTCTGCATCTTCAGGGGAGAAAGTTCACCATGACCTGCAGTGGCAGCTTCAAGT	483
Oy	481	ATAAGTTACATGCACCTGGTACCAAGCAAGAAAGCTGTCACTCCCCCAAAAGATGATTTAT	540
Db	484	GTAAGTTACATGCACCTGGTCCAGAGCAAGCAAGGCACTTCTCCAAACTGTGATTTAT	543
Oy	541	GACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCTTTCAGTGGCAGTGGGTCTGGAGCC	600
Db	544	AGCACATCCAACTGGCTTCTGGAGTCCCTGCTCGCTTTCAGTGGCAGTGGGTCTGGAGCC	603
Oy	601	TCTTATTCCTCAACATCAGCAGCATGAGGCGCTGTATGATGTCGCCACTTATTACTGGCAT	660
Db	604	TCTTATTCCTCAACATCAGCAGCATGAGGCGCTGTATGATGTCGCCACTTATTACTGGCAG	663
Oy	661	CAGCGGAGTATTAACCGGCTTCAGGTTCCGGTGCCTGGGACACAGTGGAAATTAACCG	717
Db	664	CAGGAGTATTAACCGGCTTCAGGTTCCGGTGCCTGGGACACAAAGTGGAAATTAACCG	720

LOCUS	AX111695	927 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 2 from Patent WO0125415.				
ACCESSION	AX111695				
VERSION	AX111695.1				
KEYWORDS	GI:13927960				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 Cichutek,K. and Engelsaecker,M.				
AUTHORS	Gene transfer in human lymphocytes using retroviral scfv cell targeting				
TITLE	Patent: WO 0125415-A 2 12-APR-2001;				
JOURNAL	Bundesrepublik Deutschland BtR (DB)				
FEATURES	Location/Qualifiers				
Source	1..927				
ORIGIN	/organism="synthetic construct"				
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Query Match	79.3%	Score 568.4	DB 6	Length 927	
Best Local Similarity	88.0%	Pred. No. 2e-155			
Matches 630	Conservative 0	Mismatches 83	Indels 3	Gaps 1	
OY	2 AGGTGAACCTGCAGCAGTCAGGACCTGAACTGGTGNAGCTGGGCGCTCACTGAAGATAT 61				
Db	143 AGGTAACTGCAGAGAGTCAGGAGACTGAACCTTGTAAGCCCTGGGCTTCACTGAATCTGT 202				
OY	62 CCTGCAAGACTTCTGTGANACAAATTCACCTGAATACACCATGCACTGGGTGAAGAGAGCC 121				
Db	203 CTTCGAAAGCTTCTGGCTACACCTTACACAGCTACTGTGATGCTGTTGAAGCAGAGGC 262				
OY	122 ATGGAAGAAGCCTTGAGTATTTGAGGATTAATCTTAACAATGGTGGTACTAATCA 181				
Db	263 CTGCAACAAGCCTTAGTGTGATCGAGAGATTGATCTCTTGATAGTTACTAATCA 322				
OY	182 AGCAAGTTCAGGGCAAGGCCAATTCAGTCTGTAACAAGTCTTCACAGCCTTACA 241				

Db 323 ATCAAACTTCAAGGCAGAGCCACATGACCTGTAGACAACTCCTCCACCAACACTTACA 382

Qy 242 TGGAGCTCCGAGCCTGCATCTGAGGATTCTGACGTCTATTACTGTGCAGAGATACTA 301

Db 383 TGCACCTCAGACAGCTGCATCTGAGGACTCTGGCGCTTATTACTGTGCAGAAAGGACT 442

Qy 302 CGGATCCGGTTTGCTTAACTAGGGTCCAGAGGACACAGGGTCAACCGTCCCTCAGGTGAGGCG 361

Db 443 ATG---CTATGAACTACTGGGGCCAGAGGACACGTACCCGTCTCTCAAGTGAATGCG 499

Qy 362 GTTCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGGACATGGACTCACTGACTCTCCAG 421

Db 500 GTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATGGACATGGACTCACTGACTCACGAG 559

Qy 422 CAATCATGTCTGCATCTCCAGGGGAGAAAGTCAACATGACCTGGAGTGGCGACTCAAGTA 481

Db 560 CAATCATGTCTGCATCTCCAGGGGAGAAAGTCAACATGACCTGGAGTGGCGACTCAAGTA 619

Qy 482 TAAGTTACATGCACCTGTATCCAGCAGAAAGCCTGTCACTCCGCCCAAAAGATGATTAATG 541

Db 620 TAAGTTACATGCACCTGTATCCAGCAGAAAGCAGGACACTCCGCCAAAGATGATTAATG 679

Qy 542 ACAATATCCAACTGGCTTTGGGAATCCCTGTCGCTTCAATGGAGATGGGCTTGGGACT 601

Db 680 ACAATATCCAACTGGCTTTGGGAATCCCTGTCGCTTCAATGGAGATGGGCTTGGGACT 739

Qy 602 CTTATTCTCTACATCAGCAGCATGAGGCTGTAGATGTCTGCCACTTATTACTGCATC 661

Db 740 CTTATTCTCTCCCAATCAGCAGCATGAGGCTGTAGATGTCTGCCACTTATTACTGCATC 799

Qy 662 AGCGGAGTATTACCCGCTACGTTCCGTGCTGGGACACAGTGTGGAAATTAATAAGG 717

Db 800 AGCGGAGTATTACCCATGAGCGTTCCGTGAGGAGACCAAGCTGAAATTAATAAGG 855

RESULT 8					
AA839011					
LOCUS	AA839011	716 bp	DNA	linear	PAT 15-DEC-2003
DEFINITION	Sequence 1 from Patent WO03076465.				
ACCESSION	AA839011				
VERSION	AA839011.1	GI:39922521			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 other sequences; artificial sequences.				
AUTHORS	Rancourt, C., Piche, A. and Beaudin, J.1.				
TITLE	Downregulation of ca 125 tumor antigen and uses thereof				
JOURNAL	Patent: WO 03076465-A 1 18-SEP-2003;				
FEATURES	Universite de Sherbrooke (CA)				
source	Location/Qualifiers				
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	/note="VH-linker-VL portion of VK-8-1.9"				
ORIGIN					
Query Match	77.5%;	Score 555.8;	DB 6;	Length 716;	
Best Local Similarity	87.7%;	Pred. No. 1.7e-161;			
Matches 629;	Conservative 0;	Mismatches 84;	Indels 4;	Gaps 2;	
Db	1 CAGGTGAACCTGCAGACAGTCAAGACTCTGAACCTGTGTGAGACCTGGGGCTTCAGTGAAGATA	60			
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1	CAGGTCCACGTGCAGAGAGTCAAGACTCTGAACCTGTGTGAACTGGGGCTTCAGTGAAGATA	60			
Db	61 TCTGTCAAG-CTTCTGATACACATTCACCTGACTCAACAATGCACTGGGTGAACAGAGC	119			
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121	CATGAAGAGCCTTGAGTGTGAGAGTATTAATCTCTAACATGTGTGATCAATCAAC	180			
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Qy	241 ATGAGAGCTCCCGCAGGCTTGACATCTTGAGGATTTCTGCAAGCTCTATTACTGTGCAAGAGATYACT 300
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Qy	658 CATCAGCGGAGTATGTTACCCGCTCACGTTCCGATGTGTGGAGACAGTTGGAAATATAA 714
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LOCUS	AY374128 723 bp mRNA linear SYN 12-FEB-2004
DEFINITION	Synthetic construct anti-idiotypic B5 single chain variable
ACCESSION	AY374128
VERSION	AY374128.1 GI:34979267
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 723)
TITLE	Beninati,C., Arseni,S., Mancuso,G., Magliani,W., Conti,S.,
JOURNAL	Midiri,A., Blondo,C., Polonelli,L. and Teti,G.
PUBMED	Protective immunization against group B meningococci using
REFERENCE	anti-idiotypic mimics of the capsular polysaccharide
AUTHORS	J. Immunol. 172 (4), 2461-2468 (2004)
TITLE	14764718
JOURNAL	2 (bases 1 to 723)
PUBMED	Beninati,C., Arseni,S., Mancuso,G., Magliani,W., Conti,S.,
REFERENCE	Midiri,A., Blondo,C., Polonelli,L. and Teti,G.
AUTHORS	Direct Submission
TITLE	Submitted (26-AUG-2003) Pathology and Experimental Microbiology,
JOURNAL	University of Messina, Via C. Valeria, 1 (Policlinico), Messina, Me
PUBMED	I-98125, Italy
REFERENCE	Location/Qualifiers
AUTHORS	1..723

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Query Match	76.7%	Score 550.2	DB 12	Length 723
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Db 1	CAGGTGAACTGCAGCAGTCAAGACCTGAACTGTGCAAAACCTGGAGGCTTCACTGTAAGATG	60		
Qy 61	TCCTGCAAGACTTGTGAAACAAATTCACTGATACCAATGCACCTGGGTGAAGCAGAGC	120		
Db 61	TCCTGCAAGGCTTGTGATACACATTCAGTAGCTATATTATGCACTGGGTGAAGCAGAGG	120		
Qy 121	CATGAAAGAGCCCTTGAGTGGATTGAGAGTAAATTAACTCTAACAATGGTGGATCTAATAC	180		
Db 121	CTTGGGCAAGGCTTGTAGTGGATTGGACATATTATCTTTACAAATGGTGGTACTAATGAC	180		
Qy 181	AAGCAGAAAGTTCAAGAGGCAAGGCCACATTTGATAGACAAGTCTTCACAGCAGCTTAC	240		
Db 181	AATAGAAAGTTCAAAAGCCAAAGGCCACACTGACCTTCAACAATATCTTCAGACCACTTAC	240		
Qy 241	ATGAGAGCTCCGACGCTGACATCTGAGAGATTCTGCACTTATTTCTGTGCAGA-----	294		
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Qy 295	GATACCTACGGGCCCCGTTGCTTACTTACGTGGTCCAAAGAGACCAAGGTCACCGTCTCCTCAG	354		
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Qy 355	GGAGGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGGATTCGACATCGAGCTCACTCAG	414		
Db 361	GGAAGCGGTTTCAGGCGAGGTGCTCTGGCGGTGGCGGATTCGAGCATCGAGCTCACTCAG	420		
Qy 415	TCCTCAGCAATCATGTCTGCACTTCCAGGGGGAAGGTTCAACATGACTGGAATGGCAGC	474		
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Qy 475	TCAGGTAAAGTTACATGCACCTGGTACACAGAGAAAGCCTGTCACTCCCCCAAAAGATGG	534		
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Qy 535	ATTATGACACATCCAAACTGGCTTCTGAGTCCCTGCTCGCTTCAAGTGGAGTGGGCTT	594		
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Qy 655	TGCAATCAGCGAGATGATACCCGCTCAGCTTCGGTCTGTGACACACAGTTGGAATATAA	714		
Db 661	TGCAGCAGTTTACTAGTTCCTCCGTAAACGTTCCGAGGGGGGCAAGCTGGGAATATAA	720		
Qy 715	CGG 717			
Db 721	CGG 723			

DEFINITION Continuous in vitro evolution.
ACCESSION BD34870
VERSION BD34870.1 GI:33044640
KEYWORDS JP 2002515224-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS Cota, G., Hudson, P.J., Iliades, P. and Irving, R.A.
TITLE Continuous in vitro evolution
JOURNAL Patent: JP 2002515224-A 4 28-MAY-2002;
DIATECH PTY LTD
COMMENT OS Homo sapiens (human)
PN JP 2002515224-A/4
PD 28-MAY-2002
PF 07-MAY-1999 JP 2000548452
PR 08-MAY-1998 AU PP 3445
PI GREGORY COJA, PETER JOHN HUDSON, PETER ILIADES, ROBERT ALEXANDER
PI IRVING
PC C12N15/09, C12N15/01, C12P21/02, C12N15/00, C12N15/00 CC
Description of Sequence: Antipeptidic surface antigen (4C2) CC
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Best Local Similarity 85.2%; Pred. No. 6.2e-159;
Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
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LOCUS AR317194 807 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6562622.
ACCESSION AR317194
VERSION AR317194.1 GI:33696534
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 807)
AUTHORS Cota, G., Hudson, P.J., Iliades, P. and Irving, R.A.
TITLE Continuous in vitro evolution
JOURNAL Patent: US 6562622-A 4 13-MAY-2003;
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Query Match 76.4%; Score 547.6; DB 6; Length 807;
Best Local Similarity 85.2%; Pred. No. 6.2e-159;
Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
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Dd	670	ACTGGAGTAGTAACCTCCACAGTTCGGGTCTGGGACCAACAGCTGAAAATAAACGG	725
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LOCUS	Af189283	1815 bp mRNA linear SYN 23-MAR-2000	
DEFINITION		Synthetic construct chimeric single chain fragment variable	
ACCESSION	Af189283		
VERSION	Af189283.1	GI:7230485	
KEYWORDS			
SOURCE			
ORGANISM		synthetic construct	
REFERENCE		other sequences; artificial sequences.	
AUTHORS		1 (bases 1 to 1815)	
TITLE		Long,M.C., Unger,S., Mah,D.C., Jebailey,L., Mah,M.A., Masri,S.A. and Nagata,L.P. Construction and characterization of a novel recombinant single-chain variable fragment antibody against Western equine encephalitis virus	
JOURNAL		Hybridoma 19 (1), 1-13 (2000)	
MEDLINE		202293323	
PUBMED		10768836	
REFERENCE		2 (bases 1 to 1815)	
AUTHORS		Long,M.C., Unger,S., Mah,D.C.W., Jebailey,L., Mah,M.A., Masri,S.A. and Nagata,L.P. Direct Submision Submitted (23-Sep-1999) Medical Countermeasures Section, Defence Research Establishment Suffield, P.O. Box 4000, Station Main, Medicine Hat, Alberta T1A 8K6, Canada	
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JOURNAL			
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QY	121 CATGAAAGACCTTGTGAGTGTGAGGATTTATCTTAACAAATGTGTGATCTTAATAC	180			
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QY	181 AAGCAAGAGTTCAGAGGCAAGGCAAGGCAATTTGACGTGAGCAAGTCTCCAGACAGCTTAC	240			
DB	364 AATGAGAAATTCAGAGAGCAAGGCAACTGATTTGAGCAATCTTCCAGACAGGCTTAC	423			
QY	241 ATGAGAGCTCCGACCTGACATCTGAGGATTTCTGACGTATTTATCTGTGCAAGA -GATAC	299			
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ACCESSION	A97142				
VERSION	A97142.1	GI:6780530			
KEYWORDS					
SOURCE	Mus sp.				
ORGANISM	Mus sp.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 725)				
	Petril,H. and Bosslet,K.				
	BONDING MOLECULES AGAINST RECEPTOR-LIGAND-COMPLEXES				

LOCUS CO802042 811 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 27 from Patent WO2004007717.
ACCESSION CO802042
VERSION CO802042.1 GI:47058596
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Unger,C.M., Beate,G., Jensen,K.H., Zehetmeier,C., Knauer,R.,
Guelbenzu,B.L., Torella,C. and Ilag,L.U.
TITLE Proteomic screen to identify disease-related biological
molecules and inhibitors thereto
JOURNAL Patent: WO 2004007717-A 27 22-JAN-2004;
Xerion Pharmaceuticals AG (DE)
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ORIGIN

Query Match 75.2%; Score 539.2; DB 6; Length 811;
Best Local Similarity 86.2%; Pred. No. 2.6e-156;
Matches 624; Conservative 0; Mismatches 85; Indels 15; Gaps 2;

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QY 246 GCTCCGAGCCTGACATCTGAGGATCTGCACTTATTAAGTGAAGA-----GA 296
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DB 661 TTACTGCCATCAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 720
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(Without alignments)
10108.771 Million cell updates/sec

Title: US-10-075-947A-1

Perfect score: 1 caggtggaactgcagcagtc.....cacagtcggaataaacgg 717

Sequence: 1 caggtggaactgcagcagtc.....cacagtcggaataaacgg 717

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	715	99.7	717	2	AAT86309
2	715	99.7	717	6	ABA92026
3	703	98.0	1175	2	AAT86311
4	593.4	82.8	717	4	AAC85339
5	593.4	82.8	717	10	AAL51099
6	593.4	82.8	717	12	ADJ88112
7	574	80.1	726	8	ACC83315
8	574	80.1	726	13	ADT91208
9	568.4	79.3	927	5	AAF61510
10	561.4	78.3	786	13	ADT91212
11	555.8	77.5	716	10	ADT91212
12	553.2	77.2	726	6	ACC83314
13	553.2	77.2	726	13	ADT91206
14	547.6	76.4	807	13	AAZ28963
15	547.6	76.4	807	13	ADT91206
16	541.4	75.5	725	2	AAK56760
17	535.6	74.7	990	5	AAH61511
18	534.2	74.5	771	4	AAH26790
19	534.2	74.5	780	4	AAH26791
20	527.8	73.6	720	6	AAH26791

21	523.8	73.1	894	2	AAK33931	AAK33931 HBV speci
22	523.2	73.0	714	6	AAD42825	AAD42825 KDR bindi
23	521.8	72.8	850	10	ACC57515	ACC57515 Costimula
24	521.6	72.7	726	2	AAT04023	AAT04023 Anti-EGFR
25	520.6	72.6	726	2	AAT04025	AAT04025 Anti-EGFR
26	520.4	72.6	732	2	AAV23579	AAV23579 Firefly 1
27	517.8	72.2	2364	2	AAV23580	AAV23580 Antibody-
28	517.4	72.2	1797	2	AAV00687	AAV00687 Fusion ge
29	517.4	72.2	1797	3	AAI10398	AAI10398 Recombina
30	515.8	71.9	719	3	AAK60427	AAK60427 Anti-TAC
31	515.8	71.9	720	4	AAK60427	AAK60427 Anti-TAC
32	515	71.8	843	10	AAD50925	AAD50925 128 antib
33	512.6	71.5	726	2	AAT04024	AAT04024 Anti-EGFR
34	512	71.4	810	13	ADSI7526	ADSI7526 Nucleoelid
35	508	70.9	723	10	ADSI1765	ADSI1765 Anti-CEA
36	507.2	70.7	810	2	AAQ90663	AAQ90663 MFE-23 an
37	504.6	70.4	732	2	AAT04020	AAT04020 Anti-EGFR
38	504.6	70.4	732	2	AAT04026	AAT04026 Anti-EGFR
39	504	70.3	1673	4	ABK52599	ABK52599 DNA encod
40	504	70.3	1673	4	ABK49930	ABK49930 DNA encod
41	503.6	70.2	2478	2	AAK86614	AAK86614 CDNA enco
42	503	70.2	732	2	AAT04021	AAT04021 Anti-EGFR
43	502.8	70.1	1479	12	ADQ91091	ADQ91091 Antibody
44	502.8	70.1	1479	12	ADQ91105	ADQ91105 Antibody
45	502.8	70.1	1479	12	ADQ91089	ADQ91089 Antibody

ALIGNMENTS

RESULT 1
AAT86309
ID AAT86309 standard; DNA; 717 BP.
XX
AC AAT86309;
XX
DT 06-APR-1998 (first entry)
XX
DE Single chain anti-distal ganglioside GD2 antibody 5F11-scFv.
XX
KW Antibody construct; distal ganglioside; GD2; single chain Fv fragment;
KW scFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;
KW tissue imaging; target delivery; toxin; streptavidin;
KW pro-drug converting enzyme; GD2-targeted lymphocyte; ss.
XX
OS Synthetic.
XX
PN WO9734634-A1.
XX
PD 25-SEP-1997.
XX
PE 20-MAR-1997; 97WO-US004427.
XX
PR 20-MAR-1996; 96US-0013703P.
XX
PA (SLOK). SLOAN KETTERING INST CANCER RES.
XX
PI Cheung NV, Larson SM, Guo H, Rivlin K, Sadelain M;
XX WPI; 1997-479996/44.
XX
PT Recombinant single chain anti-distal ganglioside GD2 antibody - useful to
PT detect tumour cells expressing GD2 and to target therapeutic agents, e.g.
PT toxins, to such cells.
XX
PS Disclosure; Page 11; 31pp; English.
XX
CC The present sequence encodes a recombinant single chain peptide, 5F11-
CC scFv. The peptide is an antibody construct comprising the variable
CC regions of the heavy and light chains of an antibody against
CC distal ganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
CC in many tumour types including neuroblastoma, osteosarcoma and other
CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,

DE Anti-disialoganglioside GD2 single chain antibody 5F11 scFv cDNA.
XX

Db 241 ATGAGCTCCGCAGCCTGAC

Db 241 ATGAGCTCCGCAGCCTGAC

```
OY 301 ACGGTCGGTGTGCTTACTGGGTCCAAAGGACCAACGCTCACCGTCTCTCAAGTGGAGGC 360
DB 301 ACGGTCGGTGTGCTTACTGGGTCCAAAGGACCAACGCTCACCGTCTCTCAAGTGGAGGC 360
OY 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTCACTTCCA 420
DB 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTCACTTCCA 420
OY 421 GCATTCATGCTGATCTCCAGGGGAGAAAGTCACTGACCTGCACTGAGCTCAAGT 480
DB 421 GCATTCATGCTGATCTCCAGGGGAGAAAGTCACTGACCTGAGTGGAGCTCAAGT 480
OY 481 ATAGTACATGACCTGGTACAGAGAAAGCTGACCTCCCAAAAGATGATTTAT 540
DB 481 ATAGTACATGACCTGGTACAGAGAAAGCTGACCTCCCAAAAGATGATTTAT 540
OY 541 GACACATCCAAATCGGCTTCTGAGATCCCTGCTCGCTTCAGTGGCAGTGGCTGGAGCC 600
DB 541 GACACATCCAAATCGGCTTCTGAGATCCCTGCTCGCTTCAGTGGCAGTGGCTGGAGCC 600
OY 601 TCTTATTCTCTCAATACAGACAGATGAGGCTGATGCTGCCACTTATTACTCCAT 660
DB 601 TCTTATTCTCTCAATACAGACAGATGAGGCTGATGCTGCCACTTATTACTCCAT 660
OY 661 CAGCGAGTAGTACCCGCTCAGCTGGGTGGGACACAGTTGGAATAAACGG 717
DB 661 CAGCGAGTAGTACCCGCTCAGCTGGGTGGGACACAGTTGGAATAAACGG 717

RESULT 3
AAT86311
ID AAT86311 standard; DNA; 1175 BP.
XX
AC AAT86311;
XX
DT 06-APR-1998 (first entry)
XX
DE Single chain anti-disialoganglioside GD2 antibody 5F11-secFv-streptavidin.
XX
KW Antibody construct; disialoganglioside; GD2; single chain Fv fragment;
KM secFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;
KM tissue imaging; target delivery; toxin; streptavidin;
KM pro-drug converting enzyme; GD2-targeted lymphocyte; ss.
XX
OS Synthetic.
XX
FH Key
FT misc_feature
FT 1..716 Location/Qualifiers
FT /note= "a
FT /note= "encodes single chain Fv fragment of antibody
FT 5F11"
FT 717..740
FT /tag= b
FT /note= "linker sequence"
FT 741..1175
FT /tag= c
FT /note= "encodes streptavidin"
XX
XX MO9734634-A1.
XX
XX 25-SEP-1997.
XX
XX 20-MAR-1997; 97WO-US004427.
XX
XX 20-MAR-1996; 96US-0013703P.
XX
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Cheung NV, Larson SM, Guo H, Rivlin K, Sadelain M,
XX
XX WPI; 1997-47996/44.
XX
XX Recombinant single chain anti-disialoganglioside GD2 antibody - useful to
```

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PT detect tumour cells expressing GD2 and to target therapeutic agents, e.g.
PT toxin, to such cells.
XX
XX Disclosure; Page 12; 31pp; English.
PS
XX
XX The present sequence encodes a recombinant single chain peptide, 5F11-
XX secFv-streptavidin. The peptide is an antibody construct comprising the
XX variable regions of the heavy and light chains of an antibody against
XX disialoganglioside (GD2) as a single chain Fv fragment (secFv). GD2 occurs
XX in many tumours types including neuroblastoma, osteosarcoma, and other
XX soft tissue sarcomas, medulloblastoma, high grade astrocytomas,
XX melanomas and small cell lung cancer. The peptide can be detectably
XX labelled, preferably with 99m-Tc, for tissue imaging of cells expressing
XX GD2. It can also be used to target delivery of a therapeutic or pre-
XX therapeutic agent, such as a toxin, streptavidin (e.g. present sequence)
XX or a pro-drug converting enzyme, to cells expressing GD2. The peptide may
XX further comprise CD8 to facilitate the formation of GD2-targeted
XX lymphocytes. T cells containing the peptide can also be used to target
XX GD2-producing tumour cells
XX
SQ Sequence 1175 BP; 276 A; 346 C; 330 G; 221 T; 0 U; 2 Other;
Query Match 98.0%; Score 703; DB 2; Length 1175;
Best Local Similarity 99.9%; Pred. No. 3.5e-189;
Matches 716; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 CAGGTGAATCTGCAGCAGCTGAGACTGATGAGGCTTCAAGTGAAGTA 60
DB 1 CAGGTGAATCTGCAGCAGCTGAGACTGATGAGGCTTCAAGTGAAGTA 60
OY 61 TCTGCAAGACTTGTGAMCAATCTCAATGATACACATGCTGAGTGAAGATA 120
DB 61 TCTGCAAGACTTGTGAMCAATCTCAATGATACACATGCTGAGTGAAGATA 120
OY 121 CATGAAAGACCTTGAAGTGAATGATTAATCTTAACAATGCTGATCACTAC 180
DB 121 CATGAAAGACCTTGAAGTGAATGATTAATCTTAACAATGCTGATCACTAC 180
OY 181 AAGCAAGATTCAGAGGCAAGGCCATTTGACTGATGACAGTCTCCAGACAGCTAC 240
DB 181 AAGCAAGATTCAGAGGCAAGGCCATTTGACTGATGACAGTCTCCAGACAGCTAC 240
OY 241 ATGAGGCTCCGACCTGACATCTGAGATTTGACAGTCTTCACTGCAAGAGTACT 300
DB 241 ATGAGGCTCCGACCTGACATCTGAGATTTGACAGTCTTCACTGCAAGAGTACT 300
OY 301 ACGTCCGTTTGTCTACTGGGTCCAAAGGACCAAGCTCAAGCTCTCAAGTGAAGC 360
DB 301 ACGTCCGTTTGTCTACTGGGTCCAAAGGACCAAGCTCAAGCTCTCAAGTGAAGC 360
OY 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTTCCA 420
DB 361 GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTTCCA 420
OY 421 GCATTCATGCTGATCTCCAGGGGAGAAAGTCACTGACCTGAGTGGAGCTCAAGT 480
DB 421 GCATTCATGCTGATCTCCAGGGGAGAAAGTCACTGACCTGAGTGGAGCTCAAGT 480
OY 481 ATAGTACATGACCTGGTACAGAGAAAGCTGACCTCCCAAAAGATGATTTAT 540
DB 481 ATAGTACATGACCTGGTACAGAGAAAGCTGACCTCCCAAAAGATGATTTAT 540
OY 541 GACACATCCAAATCGGCTTCTGAGATCCCTGCTCGCTTCAGTGGCAGTGGCTGGAGCC 600
DB 541 GACACATCCAAATCGGCTTCTGAGATCCCTGCTCGCTTCAGTGGCAGTGGCTGGAGCC 600
OY 601 TCTTATTCTCTCAATACAGACAGATGAGGCTGATGCTGCCACTTATTACTCCAT 660
DB 601 TCTTATTCTCTCAATACAGACAGATGAGGCTGATGCTGCCACTTATTACTCCAT 660
OY 661 CAGCGAGTAGTACCCGCTCAGCTGGGTGGGACACAGTTGGAATAAACGG 717
DB 661 CAGCGAGTAGTACCCGCTCAGCTGGGTGGGACACAGTTGGAATAAACGG 716
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	RESULT	4
ID	AAC85539 standard; DNA; 717 BP.	
XX AC	AAC85539;	
XX DT	04-JUN-2001 (first entry)	
XX DE	sCFv 508F coding sequence.	
XX KM	Human; prion protein; plaque forming disease; display vehicle; kuru; aggregating protein; amyloid plaque; brain; early onset; senility; Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis; hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD; bovine spongiform encephalopathy; Creutzfeldt-jakob Disease; FRI; Gerstmann-Strausner-Sheinker Disease; GSS; fatal familial insomnia; antibody; ss.	
XX OS	Synthetic.	
PX PN	WO200118169-A2.	
XX PD	15-MAR-2001.	
PX PF	31-AUG-2000; 2000WO-IL000518.	
PX PR	03-SEP-1999; 99US-0152417P. 29-DEC-1999; 99US-00473653.	
PX PR	31-JUL-2000; 2000US-00629971.	
PX PA	(UTRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.	
XX PI	Solomon B, Frenkel D, Hanan E;	
XX DR	WPI; 2001-244564/25. P-PADB; AAB47111.	
PT PT	Treating amyloidalgenic disease such as Alzheimer's disease, BSE or CJD comprises presentation of plaque derived antigens or epitopes on a display vehicle, and introducing the vehicle into the recipient.	
PX PS	Example 2; Fig 11; 120pp; English.	
CC CC	This sequence encodes scfv 508F heavy chain, linker and light chain. The scfv fragment was derived from the 508 Igm hybridoma which is generated from splenocytes of a mouse that has been immunised with a peptide corresponding to the 16 amino terminal residues of beta-AP conjugated to keyhole limpet hemocyanin used a carrier. The resultant variable chain fragments may be used in the method of the invention. Cys 96 of the VL fragment was replaced with various amino acids to see if production yield or stability were effected without having an adverse effect on its binding affinity. The invention provides an agent for treating a plague forming disease. Antigenic polypeptides are displayed on a display vehicle and are capable of eliciting antibodies capable of disaggregating the aggregating protein and/or of preventing aggregation of the aggregating protein. This reduces formation of amyloid plaques in the brain of victims of plaque forming diseases, e.g. early onset Alzheimer's disease, late onset Alzheimer's disease, pre-symptomatic Alzheimer's disease, SAA amyloidosis, hereditary Icelandic syndrome, senility, multiple myeloma, scrapie, bovine spongiform encephalopathy (BSP), kuru, Creutzfeldt-Jakob Disease (CJD), Gerstmann-Streusler-Sheinker Disease (GSS) and fatal familial insomnia (FFI).	
SO SO	Sequence 717 BP; 178 A; 174 C; 198 G; 167 T; 0 U; 0 Other;	
	Query Match 82.8%; Score 593.4; DB 4; Length 717;	
	Best Local Similarity 90.1%; Pred. NO. 4e-158;	
	Matches 646; Conservative 0; Mismatches 66; Indels 3; Gaps 1,	
GQ	CAGGTGAATCTGCACACTCAAGACCCTGGAACTTGTTGCGGCCCTTCAGTGAAGAATA 60	

Db	1	CAGGTCAAACTGCAAGAGTCAAGGGCTAGCTGTGGAGGCGCTGGGGTCTCACTGAAGATT	60
Qy	61	TCCTGCAAGACTTCTGAMACAAATTCATGAATAACCAATGCACTGGGTGAAGCAGAC	120
Db	61	TCCTGCAAGGGTTCGGCTACACATTCACTGATATATGATATGCACTGGGGTGAAGCAGAGT	120
Qy	121	CATGAAAAGAGCTTGAGTGGATTGGAGATATTAATCTCAACAATGGTGGTACTAATCTAC	180
Db	121	CATGAAAAGAGCTTAGAGTGGATTGGAGATATTAATGATTAATTAATGATGATGATCTAGCTAC	180
Qy	181	AAGCAGAAGTTCAAAGGGCAGAGCCACATTTAGACTGTAGACAAAGTCTCCAGCAGGCTTAC	240
Db	181	AACCAAGATTTCAGGGGCAAGGCCAACATGACTGTAGACAAATCTCTCCAGCAGGCTTAT	240
Qy	241	ATGAGACTCCGCAAGCCTGACATCTGAGGATTTCTGCAAGTCTATTAATCTGTGCAAGA--GAT	297
Db	241	ATGGAATCTTGCCAGACTGACATCTGAGGATTTCTGCAATCTATTAATCTGTGCAAGAAGGCT	300
Qy	298	ACTAAGGTCCCGTTTGGCTTAATCTGGGTTCCAAGGACACAGGTCAAGCTCTCTCAAGTGA	357
Db	301	ACTATGTCTCTACTTTGACTACTGGGGCCAAAGTGAACCAAGGTCAACGCTCTCTCAAGTGA	360
Qy	358	GGCGGTTCAAGGGGAGGTGGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTAGTCT	417
Db	361	GGCGGTTCAAGGGGAGGTGGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTAGTCT	420
Qy	418	CCAGCAATCATGTCTGCATCTTCCAGGGGAGAAAGTCAACATGACCTGCAGTGGCAGCTCA	477
Db	421	CCAGCAATCATGTCTGCATCTTCCAGGGGAGAAAGTCAACATGACCTGCAGTGGCAGCTCA	480
Qy	478	AGTATTAAGTTACATGCATCTGGTACCAAGCAAGAGCTGTACCTCCCCCAAAAGATGGATT	537
Db	481	AGTATTAAGTTACATGCATCTGGTATGAGCAAGAGCCAGGACCTCCCCCAAAAGATGGATT	540
Qy	538	TATGACACATCCAAACTGAGTCTTGGAGTCCCTGTGCTGCTTCAATGAGCAGTGGGATCTGGG	597
Db	541	TATGACACATCCAAACTGAGTCTTGGAGTCCCTGTGCTGCTTCAATGAGCAGTGGGATCTGGG	600
Qy	598	ACCTCTTATTTCTTCAACATCAGCAGCATGAGAGCTGTATGATGTCCCACTTATTAATCTGC	657
Db	601	ACCTCTTATTTCTTCAACATCAGCAGCATGAGAGCTGTATGATGTCCCACTTATTAATCTGC	660
Qy	658	CATCAGCGGAGTGAATTAACCGCTCACGTTCCGCTGCTGGACACAAGTTGGAAATTAATA	714
Db	661	CATCAGCGGAGTGAATTAACCCCAATTCAGTTCCGAGGGGGGCCAAGCTGGAAATTAATA	717
RESULT 5			
AAL51099			
XX	ID	AAL51099 standard; DNA; 717 BP.	
XX	AC	AAL51099;	
XX	DT	27-FEB-2003 (first entry)	
DE		Human neurological/CNS disease treatment method-related gene.	
XX			
KW		Gene; de; vaccine; gene therapy; neurological disease; CNS disorder;	
KW		central nervous system disorder; olfactory system; Alzheimer's disease;	
KW		Creutzfeldt-Jakob disease; Huntington's chorea; Parkinson's disease;	
KW		viral infection of the brain; brain tumour; lysosomal storage disease;	
XX		multiple sclerosis.	
XX	OS	Homo sapiens.	
XX	PN	WO200274243-A2.	
XX	PD	26-SEP-2002.	
XX	PF	15-MAR-2002; 2002MO-US008042.	
XX	PR	15-MAR-2001; 2001US-00808037.	
XX			

PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 PA (MCIN/) MCINNIS P.
 XX
 XX Solomon B, Frenkel D;
 XX WPI; 2003-040542/03.
 DR P-PSDB; MA016066.
 XX
 PT Treating or diagnosing neurological diseases of the central nervous
 PT system, e.g. Alzheimer's disease, comprises displaying a polypeptide or
 PT diagnostic agent on viral display vehicle and introducing or detecting
 PT the display vehicle.
 XX
 XX Example 2; Fig 11A; 214pp; English.
 PS
 CC The invention comprises a method for treating a neurological disease or a
 CC central nervous system (CNS) disorder. The method involves displaying a
 CC therapeutic molecule capable of treating the neurological disease or CNS
 CC disorder on a viral display vehicle. The viral display vehicle is then
 CC introduced into the olfactory system of a subject to treat the disease or
 CC disorder. The method of the invention is useful for preventing, treating
 CC and diagnosing neurological diseases or CNS disorders, such as:
 CC Alzheimer's disease; Creutzfeldt-Jakob disease; Huntington's chorea; viral
 CC infections of the brain; brain tumours; lysosomal storage diseases;
 CC Parkinson's disease; and multiple sclerosis. The present DNA sequence
 CC represents a gene which was used in the invention
 XX
 SQ Sequence 717 BP; 178 A; 174 C; 198 G; 167 T; 0 U; 0 Other;
 Query Match 82.8%; Score 593.4; DB 10; Length 717;
 Best Local Similarity 90.1%; Pred. No. 4e-158;
 Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
 QY 1 CAGGTGAACCTGACAGCACTGAGCTGAGTGAAGCTGCGGCTTCACTGAGTAA 60
 DB 1 CAGGTGAACCTGACAGCACTGAGCTGAGTGAAGCTGCGGCTTCACTGAGTAA 60
 QY 61 TCCTGCAAGACTTCTGGANACAAATTCTGATACACAGCACTGGGTGAAGAGC 120
 DB 61 TCCTGCAAGACTTCTGGCTACACATTCATGATTAAGTATGACACTGGGTGAAGAGC 120
 QY 121 CATGAAAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 DB 121 CATGAAAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 QY 181 AAGCAAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 DB 181 AAGCAAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 QY 241 ATGAGAGCTGCGGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 297
 DB 241 ATGAGAGCTGCGGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
 QY 298 ACTACGGTCCCGTGGTCTTACTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
 DB 298 ACTACGGTCCCGTGGTCTTACTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
 QY 301 ACTATGCTCTTACTTGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 DB 301 ACTATGCTCTTACTTGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 361 GGGCGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 DB 361 GGGCGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 QY 418 CCACAGATCATGTCGATCTCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
 DB 418 CCACAGATCATGTCGATCTCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
 QY 421 CCACAGATCATGTCGATCTCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 DB 421 CCACAGATCATGTCGATCTCCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 QY 478 AGTATTAAGTTCATGACCTGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 537
 DB 478 AGTATTAAGTTCATGACCTGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 537
 QY 481 AGTATTAAGTTCATGACCTGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 DB 481 AGTATTAAGTTCATGACCTGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 QY 538 TATGACACATCAAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGGAGGAGGAGGAGGAG 597
 DB 538 TATGACACATCAAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGGAGGAGGAGGAGGAG 597
 QY 541 TATGACACATCAAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGGAGGAGGAGGAGGAG 600
 DB 541 TATGACACATCAAACTGGCTTCTGAGAGTCCCTGCTGCTTCACTGAGGAGGAGGAGGAGGAG 600

QY 598 ACCTCTTATTTCTACATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657
 DB 601 ACCTCTTATTTCTACATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 658 CATGAGCGGAGTGAAGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
 DB 661 CATGAGCGGAGTGAAGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
 RESULT 6
 ADJ88112
 ID ADJ88112 standard; DNA; 717 BP.
 XX
 AC ADJ88112;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human beta amyloid peptide antibody (508) heavy chain DNA.
 XX
 KW Neurological disease; central nervous system; CNS disorder;
 KW plaque-forming disease; Alzheimer's disease; SAA amyloidosis;
 KW hereditary Icelandic syndrome; senility; multiple myeloma; scrapie;
 KW bovine spongiform encephalopathy; BSE; kuru; Creutzfeldt-Jakob disease;
 KW CJD; Gerstmann-Sträussler-Scheinker disease; GSS; fatal familial insomnia;
 KW FFI; non-plaque-forming disease; Huntington's chorea; viral infection;
 KW brain tumour; lysosomal storage disease; neurodegeneration;
 KW multiple sclerosis; vaccine; beta amyloid peptide; beta AP; antibody;
 KW human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 XX Key 1..717
 FT /*tag= a
 FT /product= "508 antibody heavy chain protein"
 FT /partial
 FT /note= "No start and stop codon"
 XX
 PN US2004013647-A1.
 XX
 PD 22-JAN-2004.
 XX
 PF 11-MAR-2003; 2003US-00384788.
 XX
 PR 03-SEP-1999; 99US-0152417P.
 PR 29-DEC-1999; 99US-00473653.
 PR 31-JUL-2000; 2000US-00629971.
 PR 31-AUG-2000; 2000WO-11000518.
 PR 15-MAR-2001; 2001US-00808037.
 PR 07-AUG-2001; 2001US-00830954.
 PR 12-APR-2002; 2002US-03171735P.
 PR 06-JUN-2002; 2002US-00162889.
 XX
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 XX
 PI Solomon B, Frenkel D;
 DR WPI; 2004-108188/11.
 DR P-PSDB; ADJ88113.
 XX
 PT Treating neurological disease CNS e.g., Alzheimer's disease, by
 PT displaying therapeutic molecule capable of treating the disease on viral
 PT display vehicle which is then administered to subject through olfactory
 PT system.
 XX
 PS Example 2; SEQ ID NO 5; 68pp; English.
 CC The invention relates to a method of treating a neurological disease or
 CC disorder of the central nervous system (CNS). The method involves
 CC displaying a therapeutic molecule capable of treating the neurological
 CC disease or disorder of the CNS on a viral display vehicle and introducing
 CC the viral display vehicle into a subject by applying an effective amount of
 CC the viral display vehicle displaying the therapeutic molecule to an


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QY 121 CATGAAAGAGCTTGAAGGATTTGAGTATTAATCCAAATGATGTTACTAATAC 180
DB 127 CTTGGGAGGGCTTTGAGTATGATATTAATCTTAAATGAATGATCTAAGTAC 186
QY 181 AAGCAGAAGTTCAAGGGGCAAGGCCACATTTGACTGATGACAACTCTCCAGCAGACCTTAC 240
DB 187 AATGAGAAGTTCAAGGGGCAAGGCCACATTTGACTGATGACAACTCTCCAGCAGACCTTAC 246
QY 241 ATGAGCTCCGAGCTTGAATCATCTGAGATTTCTGCAATCTTATCTGTCAGAA--GAT 297
DB 247 ATGAGCTCCGAGCTTGAATCATCTGAGATTTCTGCAATCTTATCTGTCAGAAATTTGAT 306
QY 298 ACTAGCGTCCGTTTGTCTTACTGAGGTCGAGGAGACAGGTCACCTGCTCCAGAGTGA 357
DB 307 AACTAGGCTGCTTTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 366
QY 358 GCGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
DB 367 GCGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426
QY 418 CCAGCAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
DB 427 CCAACAAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
QY 478 AGTAAAGTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
DB 487 AGTAAAGTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
QY 538 TATGACATCATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
DB 547 TATGACATCATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 598 ACCTTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
DB 607 ACCTTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
QY 658 CATGACGAGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
DB 667 CAACAGTGAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726

RESULT 8
ADT91208
ID ADT91208 standard; DNA; 726 BP.
XX
AC ADT91208;
DT 16-DEC-2004 (first entry)
XX
DE Single chain variable fragment (scfv) antibody encoding DNA #2.
XX
KW Tumour; benign intracranial meningioma; arteriovenous malformation;
KW angioma; macular degeneration; melanoma; adenocarcinoma;
KW malignant glioma; prostatic carcinoma; kidney carcinoma;
KW bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KW lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
KW liver carcinoma; breast carcinoma; ovarian carcinoma; angiolipoma;
KW retrofetal fibroplasia; haemangioma; Kaposi's sarcoma;
KW single chain variable fragment; scfv; gene; ds.
XX
OS unidentified.
XX
FH Key Location/Qualifiers
FT 1..726
FT CDS
FT /*tag= a
FT /product= "Single chain variable fragment (scfv)
FT /antibody=
FT /partial
FT /note= "No stop codon"
XX
XX US2004191249-A1.
```

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PD 30-SEP-2004.
XX
XX 20-OCT-2003; 2003US-00689006.
XX
XX 28-APR-2000; 2000WO-US011485.
PR 09-NOV-2001; 2001US-00914605.
PR 27-SEP-2002; 2002US-00259087.
XX
PA (UVA-) UNIV VANDERBILT.
XX
PI Hallahan DE, Mernaugh R;
XX
DR WPI; 2004-698661/68.
DR P-PSDB; ADT91209.
XX
XX Screening phage-displayed antibodies binding to radiation-inducible
PT neointigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.
XX
PS Claim 4; SEQ ID NO 19; 64pp; English.
XX
XX The invention relates to a method for screening phage-displayed
CC antibodies binding to radiation-inducible neointigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phage-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neointigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, angioma,
CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumours, solid tumour metastases, angiolipomas,
CC retrofetal fibroplasias, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a DNA encoding single chain variable fragment (scfv)
CC antibody that binds to radiation-inducible neointigens.
XX
SQ Sequence 726 BP; 177 A; 183 C; 201 G; 165 T; 0 U; 0 Other;

Query Match
Best Local Similarity 80.1%; Score 574; DB 13; Length 726;
Query Match 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

QY 1 CAGGTGAAGTTCAGAGCTGAGACCTGAATGCTGAGGAGGCTTCAAGTAAATGA 60
DB 7 CAGGTGAAGTTCAGAGCTGAGACCTGAATGCTGAGGAGGCTTCAAGTAAATGA 66
QY 61 TCTGCAAGACTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 67 TCTGCAAGACTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 126
QY 121 CATGAAAGAGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 127 CTTGGGAGGGCTTTGAGTATGATATTAATCTTAAATGAATGATCTAAGTAC 186
QY 181 AAGCAGAAGTTCAAGGGGCAAGGCCACATTTGACTGATGACAACTCTCCAGCAGACCTTAC 240
DB 187 AATGAGAAGTTCAAGGGGCAAGGCCACATTTGACTGATGACAACTCTCCAGCAGACCTTAC 246
QY 241 ATGAGCTCCGAGCTTGAATCATCTGAGATTTCTGCAATCTTATCTGTCAGAA--GAT 297
DB 247 ATGAGCTCCGAGCTTGAATCATCTGAGATTTCTGCAATCTTATCTGTCAGAAATTTGAT 306
QY 298 ACTAGCGTCCGTTTGTCTTACTGAGGTCGAGGAGACAGGTCACCTGCTCCAGAGTGA 357
DB 307 AACTAGGCTGCTTTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 366
QY 358 GCGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
DB 367 GCGGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426
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Dy 662 AGCGGAGTAGTTACCCGGCTCACCGTTCGGTGTGGGCACAGTTGGAAATAAAAA
800 AGCGGAGTAGTTACCCCATGACGTTCCGTTGAGGAGCAAGCTTGGAATAAAAAA
Db 855

RESULT 10
ADT91212
ID ADT91212 standard; DNA; 786 BP.

KW Tumour, benign intracranial meningioma; arteriovenous malformation
KW angiona; macular degeneration; melanoma; adenocarcinoma;
KW malignant glioma; prostatic carcinoma; kidney carcinoma;
KW bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KW lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma
KW liver carcinoma; breast carcinoma; ovary carcinoma; angiolipoma;
KW retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
KW single chain variable fragment; scfv; gene; ds.

OS Unidentified.

Key	Location/Qualifiers
EH	1..786
FT	/*tag= a
FT	/product= "Single chain variable fragment (scFv)
FT	antibody"

PN US2004191249-A1.

PD 30-SEP-2004.

PF 20-OCT-2003; 2003US-00689006.

PR 28-APR-2000; 2000WO-US011485.

PR 27-SEP-2002; 2002US-00259087.

PA (UYVA-) UNIV VANDERBILT.

PI Hallahan DE, Mernaugh R

DR WPI; 2004-698661/68.

PT Screening phage-displayed antibodies binding to radiation-inducible
PT neointigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.

PS Claim 4; SEQ ID NO 23; 64pp; English

CC The invention relates to a method for screening phase-displayed
CC antibodies binding to radiation-inducible neointigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phase-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neointigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, angiooma,
CC meningioma, glioma, melanoma, adenocarcinoma, malignant glioma,
CC metastatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumours, solid tumour metastases, angiofibromas,
CC rarerolental fibroplasts, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a DNA encoding single chain variable fragment (scFv)
CC antibody that binds to radiation-inducible neointigens.

XX Sequence 786 BP; 185 A; 200 C; 224 G; 177 T; 0 U; 0 Other
SQ

Query Match#	78.3%	Score 561.4	DB 13	Length 786
Best Local Similarity	87.0%	Pred. No. 5.1e-149		
Matches 629, Conservative	0	Mismatches 88	Indels 6	Gaps 1

QY	1	CAGGGAACCTGCAGCAGTCAAGGACCTGAACTGATGTMAGCCCTGGGGCTTCAGTGAAGATA	60
Db	7	CAGGTGAAGCTGCAGCAGTCTGGACTTGAAGCTGGTGAAGCCCTGGGGCTTCAGTGAAGATG	66
QY	61	TCCTGCAAGACTTCGTGANAACAATTCACTGAATACACATGCACTGGGTGAAGCAGAGC	120
Db	67	TCCTGCAAGCCTTCGTGATACACATTTCACTGACTGATGTATGACATCGGGTGAAGCAGAGC	126
QY	121	CATGGAAGAGCCTTGAGTGGATTGGAAGTATTAATCCCAAGATGATGTTACTATC	180
Db	127	AATGGAAGAAGCTTGAGTGGATTGGAAGTATTAATGATTCCTTACTATGATGTTACTATC	186
QY	181	AAGCAGAAGTTCAGAGGCAAGGCCACATTTGACTGTAGAACAAGTCTCCAGCAAGCCTAC	240
Db	187	AACAGAAAGTTCAAGGGCAAGGCCACATTTGACTGTAGAACAATTCCTCCACACAGGCTAC	246
QY	241	ATGGAAGTCCGCAAGCTCTGACATCTGAGAGATTCTGCAGTCTATTACTGTGCAAGA-----	294
Db	247	ATACAGCTTCAGAGAGCTGACATCTGAGACTCTGAGTCTATTAATGTGCAAGATGGAT	306
QY	295	GATACCTACGGTCCCGTTGCTTACTAGGATCCAAAGGACCAAGCAGTCAAGCTCTCAGGT	354
Db	307	GATTACTACGAGAGGTTTTCTTACTTGGGCCAAAGGACCAATGGTCAAGCTCTCCTCAGGT	366
QY	355	GGAGGCGGTTCAAGCGAGGTGGCTCTGGCGGTGGCGATCGGACATCGAGTCACTCAG	414
Db	367	GGAGGCGGTTCAAGCGAGGTGGCTCTGGCGGTGGCGATCGGACATCGAGTCACTCAG	426
QY	415	TCTCCAGAAATCATGCTTCGCATCTCCAGGGGAGAAAGTCAACATGACTCGAGTGGCAGC	474
Db	427	TCTCCAGAAATCATGCTTCGCATCTTCAGGGAGAAAGTCAACATGACTCGAGTGGCAGC	486
QY	475	TCAAGTATGAGTTACATGCACTGTATACAGCAGAAAGCCTGTCACTTCCCCAAAGATGG	534
Db	487	TCAATATGAAAGTACATGTAAGTATACAGCAGAAAGTCAAGTGGCTCCCCAAACTATGG	546
QY	535	ATTATATGACATCCAACTGGCTTCTGGAATCCCTGCTCGCTTCAGTGGCAATGGGTCT	594
Db	547	ATTATATGACATCCAACTGGCTTCTGGAATCCCAAGCTCGCTTCAGTGGCAATGGGTCT	606
QY	595	GGGAGCTCTTAATTCCTCACAATCAGACATGAGAGGCTGTAGATCTCCACTTATTAAC	654
Db	607	GGGAGCTCTTAATTCCTCACAATCAGACATGAGAGGCTGTAGATCTCCACTTATTAAC	666
QY	655	TGCCATCAGCGGAGTGAATCCCGCTCAACGTTCCGTGCTGGGACACAGTTGGAAATAAA	714
Db	667	TGCCAGCAGTTTACAGTTCCTCCCGTATACGTTCCGATCCGGGACCAAGGCTGGAAATCAA	726
QY	715	CGG 717	
Db	727	CGG 729	
RESULT 11			
ADC79233			
ID	ADC79233	standard; DNA; 716 BP.	
XX	ADC79233;		
AC	01-JAN-2004	(first entry)	
XX			
DT	VK-8-1.9	scFv nucleotide sequence SEQ ID NO:1.	
XX			
CA	CA 125	tumour antigen; CA 125 tumour antigen modulator;	
CM	CA 125	tumour antigen-associated disease; cytostatic; gene therapy; gene;	
de			

XX	Synthetic.
OS	
XX	
PN	WO2003076465-A2.
XX	
PD	18-SEP-2003.
XX	
PF	11-MAR-2003; 2003WO-CA000341.
XX	
PR	11-MAR-2002; 2002US-0363306P.
XX	
PR	28-FEB-2003; 2003CA-02420494.
XX	
PA	(UYSH) UNIV SHERBROOKE.
XX	
FI	Rancourt C, Piche A, Beaudin J;
DR	WPI, 2003-722323/68.
XX	
PT	New modulator capable of negatively modulating a CA 125 tumor antigen in
XX	a mammalian cell, useful for preparing a composition for preventing or
PT	treating CA 125 tumor antigen-associated disease in a mammal.
XX	
PS	Claim 7; SEQ ID NO 1; 90pp; English.
XX	
CC	The present invention describes a modulator capable of negatively
CC	modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC	(1) a recombinant nucleic acid comprising at least one sequence selected
CC	from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC	ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC	acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC	or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC	negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC	modulator capable of negatively modulating a CA 125 tumour antigen has
CC	cytostatic activity, and can be used in gene therapy. The modulator,
CC	recombinant nucleic acid, vector or host cell can be used for preparing a
CC	composition for preventing or treating CA 125 tumour antigen-associated
CC	disease in a mammal.
XX	
SEQ	Sequence 716 BP; 170 A; 191 C; 196 G; 159 T; 0 U; 0 Other;
XX	
Query Match	77.5%; Score 555.8; DB 10; Length 716;
Best Local Similarity	87.7%; Pred. No. 1.9e-147;
Matches 629; Conservative	0; Mismatches 84; Indels 4; Gaps 2.
QY	1 CAGGTGAAACTGTCAGACAGTCAGACCTGAACTGATGAGCCCTGGGGCTTCACTGAAGATA 60
DB	1 CAGGTCCAGCTCAGAGAGTCAGAGACTGAACCTGATGGAACCTGGGGCTCACTGAAGATA 60
QY	61 TCTCTGCAAGACTTCTGAGANCAAAATTCACTGAATACACCATGCACTGGGTGAAGACAGC 120
DB	61 TCTCTCAAG-CTTCTGATATCACTTCACTGACTGAACATGCACTGGGTGAAGACAGC 119
QY	121 CATGAAAGAGCCTTGAGTGATGAGAGTATTAATCTCAACAAATGATGATCTAACTAC 180
DB	120 CATGAAAGAGCCTTGAGTGATGAGAGTATTAATCTCAACAAATGATGATCTAACTAC 179
QY	181 AAGCAAGATTCAAGGGCAGAGCCCAATTGACTGTAGCAAGTCTCTCCAGCAAGACCTTAC 240
DB	180 AACCAAGATTCAAGAAACAAGGCTCTCTTGACTGTAGCAAGTCTCTCCAGCAAGACCTTAC 239
QY	241 ATGAGAGCTCCGAGCCTGACATCTGAGATTTCTGAGTCTATTACTGTGCAAGAGATACT 300
DB	240 ATGAGAGCTCCGAGCCTGACATCTGAGAGTCTGTGAGTCTATTACTGTGCAAGAGTCTG 299
QY	301 ACGGACCGG---TTTGCTTACTGGGTCCAAAGGACCAAGGTCAACGCTCTCCAGGTGGA 357
DB	300 GGGTTTGGTACTTGATGATCTCTGGGACCAAGGACCAAGGTCAACGCTCTCTCCAGGTGGA 359
QY	358 GGGCGTTACGGCGAGGTGCTCTGTGGCGGTGGCGATCGSACATCGAGCTCACTAGTCT 417
DB	360 GGGCGTTACGGCGAGGTGCTCTGTGGCGGTGGCGATCGSACATCGAATGACCAAGTCT 419
QY	418 CCAGCAATCATCTTCACAGGGGAAAGTCAACATGACCTGCAAGTGGACCTCA 477

Db	420	CCAGCAATCTGCTGCACTCTCAGAGGAGAAAGGTCAAAATGACATTGCAAGGCCACCCCA	479
Qy	478	AGTATAGATTACATGACGACTGTTACCAAGAGAAGCCTGTACCTTCCCCAAAGATGATTT	537
Db	480	AGTGAAGTTACATGACGACTGTTATCAGACGAAGAAGCAGGATCTCTCCCAAACTTGGATT	539
Qy	538	TATGAACATCCAAACTGGCTTCTTGAGATCCCTGTCTGTGCTTCATATGGCAATGGGTCTGGG	597
Db	540	TATACCAATCCAACTGGCTTCTTGAGATCCCTGTCTGTGCTTCATATGGCAATGGGTCTGGG	599
Qy	598	ACCTTTATTTCTCTCAATCAGACGACATGAGAGGCTGATGCTGCCATTATTAATGTC	657
Db	600	ACCTTTATTTCTCTCAATCAGACGACGATGAGAGGCTGATGCTGCCATTATTAATGTC	659
Qy	658	CATCAGCGGAGTATGATCCCGCTCAAGTTGGGTGCTGGGACACAGTTGGAATATAAA	714
Db	660	CACGACGTGATGTGTAGCCCAACCAAGTTGGGTGCTGCCACCAAGCTGGAATATAAA	716
RESULT 12			
ID	ACC83314	standard; DNA; 726 BP.	
XX	ACC83314;		
DT	29-AUG-2003	(first entry)	
XX			
DE	Single chain antibody encoding DNA #SEQ ID 17.		
XX			
KM	Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;		
KM	cervix; colorectum; lung; ovary; pancreas; prostate; stomach;		
KM	cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;		
KW	multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; gene;		
KM	antibody; ds.		
XX			
OS	Synthetic.		
XX			
Key	Location/Qualifiers		
FT	1..726		
FT	/*tag= a		
FT	/partial		
FT	/note= "no stop codon"		
XX			
PN	WO2003028640-A2.		
PD	10-APR-2003.		
XX			
PF	27-SEP-2002; 2002WO-US030917.		
XX			
PR	03-OCT-2001; 2001US-0328123P.		
PA	(UYVA-) UNIV VANDERBILT.		
XX			
PI	Hallahan DE, Qu S;		
XX			
DR	WPI; 2003-421186/39.		
DR	P-PSDB; ABR62131.		
PT	Identifying molecule that binds to irradiated tumor in a subject, by		
PT	exposing tumor to ionizing radiation, administering library of diverse		
PT	molecules and isolating library molecules from tumor to identify the		
XX	target.		
PS	Claim 38; Page 104-105; 108pp; English.		
XX			
CC	The invention relates to a method for identifying a molecule that binds		
CC	an irradiated tumor in a subject. The method of the invention involves		
CC	exposing a tumor to ionizing radiation, administering a library of		
CC	diverse molecules to a subject, and isolating one or more molecules of		
CC	the library from the tumor. The method of the invention is useful for		
CC	identifying a molecule that binds an irradiated tumour in a subject e.g.		
CC	warm-blooded vertebrate and human, and also for tumour detection. The		

CC tumour is a primary or a metastasized tumour such as carcinoma of the
 CC bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
 CC stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
 CC multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
 CC method of the invention is useful for X-ray-guided delivery of a
 CC therapeutic composition, a diagnostic composition or their combinations
 CC to a tumour in a subject. The current sequence represents a single chain
 CC antibody encoding sequence that was identified following *in vivo* panning
 CC to irradiated tumours. This antibody binds P-selectin

XX Sequence 726 BP, 173 A, 188 C, 202 G, 163 T, 0 U, 0 Other;

Query Match 77.2%; Score 553.2; DB 8; Length 726;

Best Local Similarity 86.4%; Pred. No. 1,1e-146; Mismatches 95; Indels 3; Gaps 1;

Matches 622; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 CAGGTGAAGTGCAGCAGTGCAGACCTGAACTGTGTGAGGCTTCAAGTGAAGATA 60
 DB 7 CAGGTGAAGTGCAGCAGTGCAGACCTGAACTGTGTGAGGCTTCAAGTGAAGATA 66
 QY 61 TCCGCAAGAGCTTCTGGANACAAATTCATCAATACACATGCACTGGGTGAACAGAC 120
 DB 67 TCTGCAAGAGCTTCTGGCTACATCACTGACTACATGATGATGATGATGATGATG 126
 QY 121 CATGAAAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 180
 DB 127 CTTGCAAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 186
 QY 181 AAGCAAGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 DB 187 AATCAAAAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246
 QY 241 ATGAGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 297
 DB 247 ATGAGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 306
 QY 298 ACTAGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
 DB 307 TACTATAGCGGATTTGATTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 366
 QY 358 GGGGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
 DB 367 GGGGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426
 QY 418 CAGCAATCATGTCTGCATCTCCAGGGAGAGAGTCACTCATGACCTGAGGAGGAGTCA 477
 DB 427 CCAACAACTCATGTCTGCATCTCCAGGGAGAGAGTCACTCATGACCTGAGGAGGAGTCA 486
 QY 478 AGTATAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537
 DB 487 AGTATAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
 QY 538 TATGACATCTCAAACTGCTTCTGAGATCCCTGCTGCTTCACTGAGGAGGAGTCTGAG 597
 DB 547 TATGACATCTCAAACTGCTTCTGAGATCCCTGCTGCTTCACTGAGGAGGAGTCTGAG 606
 QY 598 ACCCTTATTTCTTCAAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657
 DB 607 ACCCTTATTTCTTCAAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666
 QY 658 CATCAGGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
 DB 667 CTGCAAGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726

RESULT 13
 ADT91206
 ID ADT91206 standard; DNA, 726 BP.

XX ADT91206;
 AC
 DT 16-DEC-2004 (first entry)

DE Single chain variable fragment (scfv) antibody encoding DNA #1.

XX Tumour; benign intracranial meningioma; arteriovenous malformation;
 KM anglioma; macular degeneration; melanoma; adenocarcinoma;
 KM malignant glioma; prostatic carcinoma; kidney carcinoma;
 KM bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
 KM lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
 KM liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
 KM retrorenal fibroplasia; haemangioma; Kaposi's sarcoma;
 KM single chain variable fragment; scfv; gene; db.

OS Unidentified.

XX Key Location/Qualifiers
 FH 1..726
 FT /tag= a
 FT /product= "single chain variable fragment (scfv)
 FT antibody"
 FT /partial
 FT /note= "No stop codon"

US2004191249-A1.

30-SEP-2004.

20-OCT-2003; 2003US-00689006.

28-APR-2000; 2000WO-US011485.

09-NOV-2001; 2001US-00914605.

27-SEP-2002; 2002US-00259087.

(UVA-) UNIV VANDERBILT.

Hallahan DE, Wernau R;

WPI: 2004-698661/68.

P-PSDB; ADT91207.

PT Screening phage-displayed antibodies binding to radiation-inducible
 PT neointigen on cell, comprises contacting cell with antibodies, treating
 PT cell with radiation, contacting cell with antibodies not binding to cell,
 PT detecting bound antibody.

PS Claim 4; SEQ ID NO 17; 64bp; English.

XX The invention relates to a method for screening phage-displayed
 CC antibodies binding to radiation-inducible neointigen on cell. The method
 CC involves contacting cell with antibodies, treating cell with radiation,
 CC contacting cell with antibodies not binding to cell and detecting the
 CC bound antibody. The method is useful for screening several phage-
 CC displayed antibodies for an ability to bind to a radiation-inducible
 CC neointigen present on a cell, where the cell is tumour cell chosen from
 CC benign intracranial meningiomas, arteriovenous malformation, anglioma,
 CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
 CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
 CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
 CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
 CC carcinoma, solid tumours, solid tumour metastases, angiofibromas,
 CC retrorenal fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
 CC carcinomas and their combinations or vascular endothelial cell. The
 CC present sequence is a DNA encoding single chain variable fragment (scfv)
 CC antibody that binds to radiation-inducible neointigens.

XX Sequence 726 BP, 173 A, 188 C, 202 G, 163 T, 0 U, 0 Other;

Query Match 77.2%; Score 553.2; DB 13; Length 726;
 Best Local Similarity 86.4%; Pred. No. 1,1e-146;
 Matches 622; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 CAGGTGAAGTGCAGCAGTGCAGACCTGAACTGTGTGAGGCTTCAAGTGAAGATA 60
 DB 7 CAGGTGAAGTGCAGCAGTGCAGACCTGAACTGTGTGAGGCTTCAAGTGAAGATA 66

Oy	61	TCCTGCAAGACTTCTTGAGAACAAATTCACTGAATAACCAATGACCTGGGTGAAGCAGAC	120		
Db	67	TCCTGCAAGGCTTCTGGCTACACATTCACATGACTACTGATGACAGTGGGTGAAGCAGAGG	126		
Oy	121	CATGAAAGAGGCTTGAGTGAATTGGAGGTATTAATCCTTAACAATGGTGGTAACTACTAC	180		
Db	127	CCTGGAACAAGGCTTGAGTGAATCGAGCGATTTGATTACTTGTGATAGTTAACTTAAGCTAC	186		
Oy	181	AAGCAAAAGTTCAAGGGCAAGGCCACATTTGACTGTAGACAAGTCTCCAGCACAGCCTAC	240		
Db	187	AATCAAAAGTTCAAGGGCAAGGCCACATTTGACTGTAGAGAAATCTCCAGCACAGCCTAC	246		
Oy	241	ATGAGAGCTCCGACAGCTGACATCTGAGGANTCTGCAGTCTATTACTGTGTC--AAAGAT	297		
Db	247	ATGACAGCTCAGACGCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAGAAGCC	306		
Oy	298	ACTACGATCCCGTTTGCTTACTAGGAGTCCAAAGGACCAAGGATCAACGATCTCTCAGGTTGA	357		
Db	307	TACTATAGGCGCATTTGATTAATTACTGAGGACCAAGGACTAACGGTCAACGATCTCTCAGGTTGA	366		
Oy	358	GGCGGTTTCAGCGGAGAGTGGCTCTGCGGGTGGCGGATTCGGAACATTCGAGCTCACTCAGTCT	417		
Db	367	GGCGGTTTCAGCGGAGAGTGGCTCTGCGGGTGGCGGATTCGGAACATTCGAGCTCAACCACTCT	426		
Oy	418	CCAGCAATCATGTCTGCGATCTCCAGGGAGAGAGTCAACATGACTGTCAGTGCAGCTCA	477		
Db	427	CCAAACAACCATGGCTGTCATCTCCAGGAGAGAGTCAACATCACTGTCGCGTGCAGCTCA	486		
Oy	478	AGTATTAAGTTAATGCACTGTGATCCGACGAAAGCCGTCAACCTCCCCCAAATAATGGANT	537		
Db	487	AGTATTAAGTTAATGCACTGTGATCCGACGAAAGTCAAGGACCTCCCCCAAACCTGGANT	546		
Oy	538	TATGACACATCCAAATCGGCTTCTGTGAGTCCCTGCTGCTGCTTCAGTGGCAGTGGGCTGGG	597		
Db	547	TATGACACATCCAAATCGGCTTCTGTGAGTCCCGATCCGATTCAGTGGCAGTGGGCTGGG	606		
Oy	598	ACCTCTTATTTCTCTCACAATCAGCAGCATGAGAGCTGTGAGTCTGCACTTAATTACTGC	657		
Db	607	ACCTCTTATTTCTCTCACAATCAGCTCCATGAGAGCTGAAGATCTGCTACTTAATTACTGT	666		
Oy	658	CATCAGCGAGATAGTAAACCGCTCAGCTTCGGTTCGGTCTGGGACACAGTTGAAATPAACGG	717		
Db	667	CTGCAGAGGATGATTAACCGGTACACGCTTGGAGTGGCCCAAGCTGGAATCAACCGG	726		
RESULT 14					
ID	AAZ28963	standard, DNA; 807 BP.			
AC	AAZ28963;				
DT	07-FEB-2000	(first entry)			
XX	Anti-Hepatitis B surface antigen (4C2) scFv encoding DNA.				
XX	Anti-hepatitis B surface antigen (4C2) scFv, single chain Fv;				
KW	light chain constant region; mouse antibody 1C3; mutation: DNA construct;				
KW	ribosome display; replicable mRNA; replication; translation;				
KW	continuous in vitro evolution; CIVE; mutant protein; diagnostic;				
XX	therapeutic property; ds.				
OS	Homo sapiens.				
XX	WO958661-A1.				
PN	18-NOV-1999.				
PD	18-NOV-1999.				
PF	07-MAY-1999; 99WO-AU000341.				
XX	08-MAY-1998; 98AU-00003445.				
XX	(DIAT-) DIATECH PTY LTD.				
PA					
XX					

PI	Cola G, Hudson PJ, Iliades P, Irving RA;
XX	
DR	WPI; 2000-039104/03.
XX	
PT	Continuous in vitro evolution of proteins by mutation, synthesis and
PT	selection of mRNA.
XX	
PS	Example 3; Fig 5d; 78pp: English.
XX	
CC	The present sequence is a DNA encoding anti-hepatitis B surface antigen
CC	(4C) scFv. It can be fused upstream of the DNA encoding light chain
CC	constant region of mouse antibody 1G3 or other gene of interest in a DNA
CC	construct, for ribosome display. The DNA construct is generated for
CC	producing replicable mRNA molecules that are used in continuous cyclic
CC	process of replication, mutation, and translation leading to continuous
CC	in vitro evolution (CITE) of mutant proteins. This method is useful for
CC	generating proteins with improved diagnostic and therapeutic properties
XX	
SEQ	Sequence 807 BP; 201 A; 207 C; 217 G; 182 T; 0 U; 0 Other;

Query Match	76.4%;	Score 547.6;	DB 3;	Length 807;
Best Local Similarity	85.2%;	Pred. No. 4.3e-145;		
Matches 610;	Conservative	0;	Mismatches 106;	Indels 0;
				Gaps 0;

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QY	62	CCTGCAGAC	CTTCTGSAANA	CAAAATTCATCTGAATACACCATGCAC	CTGGGTGAA	GACGAGACC	121
Db	70	CCTGGAAG	GGTTCCGGCTACATTCATCTGATTTATGATACATTTGGGTGGAAGCAGAGTTC				129
QY	122	ATGGAAGA	GCCCTTGAGTGTGATTTGGAGGTATTTAATCCTAACAATG	GTGTACTA	CTTCA		181
Db	130	ATGCCAA	AGTCTGTGAAGTGTGACTTATTAAGTAATTCCTTTGTGTAAATCAAACTTCA				189
QY	182	AGCAGAA	GTTCAGAGGSCAAGGCCACATTTAGCTGTAGACAGTGTCTCCAGCA	CAGCCTCA			241
Db	190	AACGAAAT	TTTGAAGGCCAAGGCCACAATATGACTGTATGACAAATTCCTCCAA	CAGGCTATT			249
QY	242	TGAGACT	CCGACGCTGACATCTGAGAGATTTCTGCAGTCTATTATCTGTGTCA	AGAGTACTA			301
Db	250	TGGAA	CTTTGGCAGATTTGACATCTGTAGAGATTTCTGCCATATATTTATCTGTCAAGA	GTATATC			309
QY	302	CGATCC	CGTTTGTACTATCTGGGTCCAAAGGGAACA	CGGTACCGTCTCTCAGGTGAGGCG			361
Db	310	ACTGAT	CTTTGATATGTCTGGGGCCAAAGGGAACA	CGGTACCGTCTCTCTCAGGTGAGGCG			369
QY	362	GTTCAG	CGGAGGTGGCTCTGGCGGTGGCGGATGGGACATGTAGCTCACTAGTTC	CCAG			421
Db	370	GTTCA	GCGGAGGTGGCTCTGGCGGTGGCGGATGGGACATTTGTGTGACCCAAATCTCCAG				429
QY	422	CAATAT	ATCTGTGCATCTCCAGGGGAGAAAGTCA	CCATACCTGTGAGTGGCAGTCA	AGTA		481
Db	430	CAATAT	ATGTGCATCTCCAGGGGAGAAAGTCA	CCATACCTGTGAGTGGCAGTCA	AGTGA		489
QY	482	TAAGTTA	CATGCATCTGTACAGCAGAAAGCTGTGCACCTCC	CCCAAAAGATGATTTATG			541
Db	490	TCAGGTAC	GTGACTGTATCCAAACGAAGTCAAGGCACTCC	CCCCAAAAGATGATTTATG			549
QY	542	ACACAT	CCAAACTGGCTTCTGAGATCCCTGTCCGTTTCAATGTGGCAGTGGGTCTGGAGCCT				601
Db	550	ACACAT	CCAAACTGGCTTCTGAGATCCCTGTCCGTTTCAATGTGGCAGTGGGTCTGGAGCCT				609
QY	602	CTTAT	CTCTCAATTCAGACAGCAATGAGAGCTGTATGTCTGCACCTTATTA	CTGCCATC			661
Db	610	CTCACT	CTCTCAATTCAGACAGCTTGGAGGCTGTAGAAATGTGTGCCACTTATTA	CTGCCAGC			669
QY	662	AGCGAG	TAGTTAACCGCTCACTGTTCCGTGTGGGACACA	GTTGGAAAT	AAAAACGG		717
Db	670	ACTGAG	ATGATACCTCTCCACGTTTCCGTGTGTGGGACCAAGCTGTGAAAT	AAAAACGG			725

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 20:10:40 ; Search time 148.31 Seconds
(without alignments)
7910.513 Million cell updates/sec

Title: US-10-075-947A-1

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Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 8181359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	715	99.7	717	3	US-09-142-974B-1
2	715	99.7	1176	4	US-09-142-974B-3
3	593.4	82.8	717	4	US-09-473-653-5
4	590.4	82.3	723	4	US-09-581-345-1
5	547.6	76.4	807	4	US-09-674-677-4
6	534.2	74.5	771	4	US-09-526-738A-1
7	534.2	74.5	780	4	US-09-526-738A-3
8	526.4	73.4	714	4	US-09-798-689-22
9	523.8	73.1	894	4	US-09-486-814A-1
10	521.6	72.7	726	2	US-08-553-487A-25
11	517.4	72.2	1797	1	US-08-463-163-2
12	515.8	71.9	719	3	US-08-279-772A-7
13	515.8	71.9	720	3	US-08-902-486-10
14	512.6	71.5	726	2	US-08-553-487A-27
15	507.2	70.7	810	2	US-08-653-507-1
16	504.6	70.4	732	2	US-08-553-487A-19
17	503	70.2	732	2	US-08-553-487A-21
18	501.6	70.0	1679	3	US-08-661-052-15
19	501.6	70.0	1679	3	US-09-186-082-15
20	501.6	70.0	1679	3	US-09-364-088-15
21	501.6	70.0	1679	3	US-09-102-716-15
22	498	69.5	1545	4	US-09-948-004-17
23	487	67.9	738	2	US-08-553-487A-23
24	471	65.7	843	3	US-09-423-439-43
25	471	65.7	1998	3	US-09-423-439-50
26	436.4	60.9	1256	3	US-09-553-498-7
27	436.4	60.9	1256	3	US-09-618-869-7

28	425.6	59.4	786	3	US-08-635-928-31	Sequence 31, Appl
29	424.4	59.2	883	4	US-09-184-658-7	Sequence 7, Appl
30	424.4	59.2	883	4	US-09-504-262D-7	Sequence 7, Appl
31	409.2	57.1	738	2	US-08-956-047-24	Sequence 24, Appl
32	403.2	56.2	777	4	US-10-092-246-7	Sequence 7, Appl
33	403.2	56.2	777	4	US-10-096-246A-7	Sequence 7, Appl
34	400	55.8	777	4	US-10-092-246-5	Sequence 5, Appl
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36	397	55.4	711	2	US-08-190-199A-64	Sequence 64, Appl
37	396.8	55.3	777	4	US-10-092-246-6	Sequence 6, Appl
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39	386.8	53.9	708	2	US-08-190-199A-60	Sequence 60, Appl
40	381	53.1	720	3	US-08-800-198-7	Sequence 7, Appl
41	381	53.1	720	3	US-09-286-595-7	Sequence 7, Appl
42	380.2	53.0	777	4	US-10-092-246-4	Sequence 4, Appl
43	380.2	53.0	777	4	US-10-096-246A-4	Sequence 4, Appl
44	377.2	52.6	774	4	US-10-092-246-3	Sequence 3, Appl
45	377.2	52.6	774	4	US-10-096-246A-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-09-142-974B-1
; Sequence 1, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Fen
; APPLICANT: Ravi, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK.P-013-USNP
; CURRENT APPLICATION NUMBER: US/09/142,974B
; CURRENT FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/US97/04427
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,703
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: 5F11-bcTv
; NAME/KEY: unsure
; LOCATION: (37)
; NAME/KEY: unsure
; LOCATION: (79)
US-09-142-974B-1
Query Match 99.7%; Score 715; DB 3; Length 717;
Best Local Similarity 100.0%; Pred. No. 3,5e+198;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CAGGTGAAGCTGACGAGCTGAGCACTGAGTGAAGCTGGGGCTTCACTGTAACATA 60
QY 61 TCCTGCAAGACTTCTGGANACAAATTCATGTAATACACATGCACTGGGTGAAGCAGAGC 120
DB 61 TCCTGCAAGACTTCTGGANACAAATTCATGTAATACACATGCACTGGGTGAAGCAGAGC 120
QY 121 CATGGAAGAGCCTTGGAGTGGATTTGAGAGTATTAATCTTAACAATGGTGTACTAATAC 180
DB 121 CATGGAAGAGCCTTGGAGTGGATTTGAGAGTATTAATCTTAACAATGGTGTACTAATAC 180
QY 181 AAGCAGAAAGTTCAAGGAGGCAAGGCAATTCATGTAACAAAGTCTTCAGACAGCCTAC 240
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Db 361 GGTTCAGGCGAGAGTGGCTCTGCGGTGCGAGATCGGACATCGAGCTCACTCACTCTCA 420
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RESULT 2
US-09-142-974B-3
; Sequence 3, Application US/09142974B
; Patent No. 6431995
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Fen
; APPLICANT: Rivlin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK.P-013-USNP
; CURRENT APPLICATION NUMBER: US/09/142,974B
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/US97/04427
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,703
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: 5P11-scFv-streptavidin
; NAME/KEY: unsure
; LOCATION: (37)
; NAME/KEY: unsure
; LOCATION: (79)
US-09-142-974B-3

Query Match 99.7%; Score 715; DB 3; Length 1176;
Best Local Similarity 100.0%; Pred. No. 4.3e-198;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 CATGGAAGAGCTTGAAGTGAATGAGAGTATTAATCTTAACAATGAGTACTAACTAC 180
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Qy 661 CAGCGAGATGATTAACCGCTCAAGTTGCTGCTGGGACACAGTTGGAATTAACCG 717
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RESULT 3
US-09-473-653-5
; Sequence 5, Application US/09473653
; Patent No. 6703015
; GENERAL INFORMATION:
; APPLICANT: Solomon, Bekka
; APPLICANT: Frenkel, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: 00/20785
; CURRENT APPLICATION NUMBER: US/09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1..1)
; OTHER INFORMATION: scFv 508f construct
US-09-473-653-5

Query Match 82.8%; Score 593.4; DB 4; Length 717;
Best Local Similarity 90.1%; Pred. No. 9e-163;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Db 241 ATGAGACTTGCAGACTGACATCTGAGGATTTGCAAGTCTTAATCTGCAAGGAGCT 300
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RESULT 4
US-09-581-345-1
Sequence 1, Application US/09581345
Patent No. 6809184
GENERAL INFORMATION:
APPLICANT: Paezan, Ira H.
APPLICANT: Chowdhury, Partha S.
APPLICANT: The Government of the United States
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Antibodies, including Fv Molecules, and
TITLE OF INVENTION: Immunocongjugates Having High Binding Affinity for
FILE REFERENCE: 015280-339100US
CURRENT APPLICATION NUMBER: US/09/581,345
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/067,175
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: WO PCT/US98/25270

PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 723
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:SS scfv
US-09-581-345-1

Query Match 82.3%; Score 590.4; DB 4; Length 723;
Best Local Similarity 89.7%; Pred. No. 6.7e-162;
Matches 646; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

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Db 4 CAGGTGAACTGCAGAGCTGAGAGCTGAGCTGGGAGCTGGGGCTTTCAGTAAAGATT 63
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Qy 535 ATTTATGACATCATCAAACTGCTTCTGAGTCCCTGCTGCTTCACTGAGGAGTGGCT 594
Db 544 ATTTATGACATCATCAAACTGCTTCTGAGTCCAGAGTGGCTTCACTGAGGAGTGGCT 603
Qy 595 GGAACCTTATCTCTCAACATGAGAGAGTGAAGCTTGAATGCTGGCACTTAATAC 654
Db 604 GGAACCTTATCTCTCAACATGAGAGAGTGAAGCTTGAATGCTGAATGCTTAATAC 663
Qy 655 TGCCATGAGGAGTATTAACCGCTCAACGCTGCTGGAGACACAGTGGAAATATAA 714
Db 664 TGCCATGAGTATTAACCGCTTCAACGCTTGGAGTGGAGTGGAGTGGAAATATAA 723
```

RESULT 5
US-09-674-677-4
Sequence 4, Application US/09674677
Patent No. 6562622
GENERAL INFORMATION:
APPLICANT: Cola, et al.
APPLICANT: CONTINUOUS IN-VITRO EVOLUTION
TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION
FILE REFERENCE: 674537-2003
CURRENT APPLICATION NUMBER: US/09/674,677

```

: CURRENT FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: PCT/AU99/00341
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: AU PP3445
: PRIOR FILING DATE: 1998-05-08
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 807
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)..(807)
: OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4c2) scFv
: Patent No. 6562622
: US-09-674-677-4

```

Query Match	76.4%	Score 547.6;	DB 4;	Length 807;
Best Local Similarity	85.2%	Pred. No. 2e-149;		
Matches 610; Conservative	0;	Mismatches 106;	Indels 0;	Gaps 0;

QY	2	AGGTGAACTCGACAGAGTGAAGACCGTGAACCTGGGGCTTCAGTGAAGAT	61
Db	10	ATGTGAAGCTTCAGAGAGTCAGGGCCTGAGCTGTGAGCCCGGGGTCTCAAGTGAAGTTA	69
QY	62	CCTGCAAGACTTCTGGANACAAATTCATCTGAATACACATGCACTGGGTGAAGAGCC	121
Db	70	CTGCAAGGGTTCGGCTCAACATTCATCTGAATTAATGCTATGCAATGGGGTGAAGAGATC	128
QY	122	ATGGAAGAAGCCCTGATGAGATTGGAAGGATTAATCTTAAACAATGGTGGTCTAATCA	181
Db	130	ATGCCAAGAGCTTAGATGATTTGAATTTATTAATTAATTCCTTGGTAAATCAACTACA	188
QY	182	AGCAGAAGTTCAGAGGCAAGGCCCAATGATCTGTAGCAAGTCTCCAGACAAGCTTACA	244
Db	190	ACCAGAAGTTTGAGGCCCAAGGCCAACAATGACTGTAGCAAAATCTCCAAACAAGCTATT	248
QY	242	TGAGAGTCCGGAGCCGTCATCTGAGAGATTCCTGCAAGTCTATTACTGTGCAAGAACTA	301
Db	250	TGGAACTTGGCAGATTGACATCTGAGAGATTCGACATCTATTACTGTGCAAGAGTATCG	309
QY	302	CGGTCCCGTTCCTACTGGGTCCAAAGGACCAAGGTACAGTCTCTCAGGTGAAGCG	361
Db	310	ACTGTCCTTTCATGTCGTGGGGCAAGGACCAAGCTCAAGCTCTCTCAAGTGAAGCG	368
QY	362	GTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATGAGGCTCACTCACTCTCCAG	421
Db	370	GTTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATGTCGTGACCAACTCTCCAG	428
QY	422	CAATCAATGTCGATCTCCAGGGGGAAGAGGTACACATGACCTGCGAGTGGAGCTCAAGTA	481
Db	430	CAATCAATGTCGATCTCCAGGGGGAAGAGGTACCAATGACCTGCGAGTGGAGCTCACTCAGTG	488
QY	482	TAAATTACATGCACTGTATCCAGCAGAAAGCTGTCACTCCCTCCCAAAAGATGATTAATG	541
Db	490	TCAGGTACGTGCACTGTATCCAAAGAGATCAGGACCTCCCTCCCAAAAGATGATTAATG	548
QY	542	ACACATCCAAACGTGGTCTTGAGATCCCTGCTGCTCAGATGGCAGTGGGTCTGGAGCT	601
Db	550	ACACATCCAAACGTGGTCTTGAGATCCCTGCTGCTCAGATGGCAGTGGGTCTGGAGCT	608
QY	602	CTTAATCTCTCAATCAACAGCAGATGAGGCTGTAGATGCTGCCATTTAATTAATGCAATC	661
Db	610	CTCACTCTCTCAACATCAGAGCTTGAAGGTGGAAGATGCTGCCATTTAATTAATGCAAGC	668
QY	662	AGCGAGTATGTAACCCGCTCAAGTTCGGGTCTGGGACAAGTTGGAAATTAAGG	717
Db	670	ACTGAGATGATTAACCTCCACAGTTCGGGTCTGGGACAAGTTGGAAATTAAGG	725

RESULT 6
US-09-526-738A-1

```

: Sequence 1, Application US/09526738A
: Patent No. 6630584
: GENERAL INFORMATION:
: APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
: APPLICANT: LTD.
: TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
: FILE REFERENCE: 1196336
: CURRENT APPLICATION NUMBER: US/09/526,738A
: CURRENT FILING DATE: 2000-03-16
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 771
: TYPE: DNA
: ORGANISM: Humanus
: US-09-526-738A-1

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Query Match	74.5%;	Score 534.2;	DB 4;	Length 771;
Best Local Similarity	84.9%;	Pred. NO. 1.6e-145;		
Matches 609;	Conservative 0;	Mismatches 105;	Indels 3;	Gaps 1;

Qy	1	CAGGTAAACTCAGACAGTCAGAGACCTGAACTGGGTGAGGCTTCAGTGAAGATA	60
Db	1	CAGGTCAACTCAGACACACTGTGGGGCTGAACTGGCAAAACCTGGGGCTCAGTGAAGATG	60
Qy	61	TCCTGCAGACCTTCTGGAGAACAAATTCACTGAATACACATGCACCTGGGTGAACGAGGC	120
Db	61	TCCTGCAGAACCTTCTGGGCTACACCTTTTACTGTGCTACGTGAATGAACCTGGGTAAAACGAGG	120
Qy	121	CATGGAAGAGCCTTAGTGAGATTGGAGGTATTAATCTTAACAATGGTGGTAACTTAAC	180
Db	121	CTGTGACAGGGTCTGGAAATGGATTGGATATCACTTAATCTTACACATGGTTATATCAAGTAC	180
Qy	181	AAGCAGAACTTCAAGGGCAAGGCCACATTTGACTGTAAACAACTCTTCAGACAAGCCTTAC	240
Db	181	AATCAGAAATTCAGAGAACAGGCCACATTTGACTGTGACCAAACTCTCAGACAGGCCCTTAC	240
Qy	241	ATGGAAGCTCCGAGGCTGACACTTGAAGATTCTGCAAGCTATTACTGTGGCAAGATACT	300
Db	241	ATGCAACTGAGACGCTGACCAATGTGAACCTTGCAGTCTATTATTGTACACTGCTTAC	300
Qy	301	ACGGTCCCGTTTGTCTTACTGGGTCCAGAGGACCAACGGTCACCGTCTCTCAGGTGAGGC	360
Db	301	TC---TTATTTTGACTACTGGGGCAAGGAGCACAGGTCACCGTCTCTCAGGTGGAGGC	357
Qy	361	GGTTCAAGGGAGGTGGCTCTTGGCGGTGGCGGAATCGACATTCGAGCTCACATCGAGTCCA	420
Db	358	GGTTCAAGGGAGGTGGCTCTTGGCGGTGGCGGAATCGACATTCGAGCTCACATCGAGTCCA	417
Qy	421	GCAATCATGTCTGCATCTCCAGGGGAGAAAGTTCACCAATGACCTTCAGTGCAGCTCAAGT	480
Db	418	GCAATCATGTCTGCATCTCCAGGGGAGAAAGTTCACCAATGACCTTCAGTGCAGCTCAAGT	477
Qy	481	ATTAAGTTACATGCACCTGGTACGACGAAGCCTGTCACTCCCTCCCAAAAGATGATTTAT	540
Db	478	GTAAATTAATCATGCACCTGGTTCACGAGAAAGCAAGCACTTCTCCAAACTCTGGATTTCT	537
Qy	541	GACATATCCAAACTGGCTTCTGGAAATCCCTGCTGAGCTTCAGTGSCAGTGGGTCTGGGACC	600
Db	538	AGCACAATCCAACTGGCTTCTGGAAATCCCTGCTGAGCTTCAGTGSCAGTGAATCTGGGACC	597
Qy	601	TCTTATTTCTCACAATCAGCAGCATGAGGCTGTGAATGCTGCACTTATCTGCTCAT	660
Db	598	TCTTATTTCTCACAATCAGCAGGATGAGGCTGAAGATGCTGCCACTTATTTATCTGCAG	657
Qy	661	CAGCGAAGATTAACCCGCTACAGTTGGGTCTGGGACACAGTTGGAAATTAACCG	717
Db	658	CAAGGAGATTAACCCATACAGTTGGAGGGGACCAAGCTGCAAATTAACCG	714

RESULT 7
US-09-526-738A-3
; Sequence 3, Application US/09526738A

Oy 541 GACACATCCAAATCGCTTCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGACC 600
 |||||
 Db 541 AGACATCCAACTGGCTTCTGAGTCCCTGCTCGCTTCAGTGGCAGTGGATCTGGACC 600
 |||||

Oy	601	TCTATTCTCTCA	CANTCAGGAG	ATGAGAGGCTGTG	AGTANCGTCCG	CACTATTACTGCAT	660
Oy	601	TCTATTCTCTCTCA	CAATCAGCGAA	TGAGAGGCTGTG	AGATGTCTCC	CACTATTACTGCAG	660
Oy	661	CAGCGAGTAGT	ATCCCGCTCA	CGTTGCGTGTG	GTGAGCA	CAGTGTGAAATATAA	714
Oy	661	CAAGGAGTAGT	ATCCCATTC	AGTTGCGCTGGG	GAGCA	CAAGCTGGAATATAA	714

RESULT 9

```

US-09-486-814A-1
; Sequence 1, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 656259910
; APPLICANT: YAMAMOTO, Hiroyo
; APPLICANT: TODOH, Naori
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486,814A
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
; FEATURE:
; OTHER INFORMATION: Clone: pZeoSV1C9
; NAME/KEY: CDS
; LOCATION: (1)..(891)
; OTHER INFORMATION: Identification Method: E
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(111)
; OTHER INFORMATION: Encoding PRE-HV sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (436)..(528)
; OTHER INFORMATION: Encoding a linker sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (838)..(891)
; OTHER INFORMATION: Encoding a TAIL sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(894)
; OTHER INFORMATION: strandedness: double-stranded
US-09-486-814A-1

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Query Match	73.1%;	Score 523.8;	DB 4;	Length 894;
Best Local Similarity	85.6%;	Pred. No. 1.8e-142;		
Matches 624;	Conservative 0;	Mismatches 84;	Indels 21;	Gaps 3;

QY	1	CAGGTGAACCTGACAGCAGTCAGGACCTGAACTGTGTGAGCCCTGGGGCTTCAGTGAAGTA	60
Db	118	CAGGTGAAGCTGCAGGAGTCCAGGACCTGAGCTGGAGGAAGCCCTGGGGCTTCAGTGAAGTA	177
QY	61	TCCGCGAAGACTTCGTGANACAAATCTACGTGAATACACATGCACTGGGTGAAGCAGGC	120
Db	178	TCCGCGAAGCCTTCGTGATCTCTGTTACTCATTCCTGCGTACACATGAACTGGGTGAAGCAGGC	237
QY	121	CATGGAAGAGCCCTTGAGTGATTTGAGGATTTAAATCCATCAATGTGTGTACTACTAC	180
Db	238	AATGGAAGAGCCCTTGAGTGATTTGAGTATATTTATCTTAAAGTGTGTACTACTAC	297
QY	181	AAGCAGAAGTTCAAGGGCAAGGCCACATTTGACTGTGACAACTCTCCAGCAGCCTAC	240
Db	298	AACCAAGAAGTTCAAGAGCAAGGCCACATTTGACTGTGACAAATCTCCAGCAGCCTAC	357

OY	241	ATGAGAGCTCCGACAGCTTGACATCTGAGAGATTCTGAGCTCTATTACTGTGCAAGAGATACT	300
Db	358	ATGCAACTGAGCAGCTTGACATCTGAGACCTCTGAGCTATTATCTGTGCAAGA-----	411
OY	301	ACGGTCCCGTTTGCTTACTGAGGGTCCAGAGGAACAAGCTCACCGTCTCTCAGGTGAGGC	360
Db	412	---CTGGGACTTGACTACTGGGGCCAGAGGACACAGCTCACCGTCTCTCAGGTGAGGC	468
OY	361	GGTTACAGCGGAGGTGGCTCTGGCGGTGGCGGATCGACATCGAGCTCACTCAGTCTCCA	420
Db	469	GGTTACAGCGGAGGTGGCTCTGGCGGTGGCGGATCGACATCGAGCTCACTCAGTCTCCA	528
OY	421	GCAATCATGTCTGCATCTTCAGGSGAGAAAGCTCACCATGACTTGCAGTGGCAGTTCAACT	480
Db	529	ACCACATGAGCTGCATCTCCGGGGAGAAAGATCACTACACTGCAGTGCACAGTCTCAAGT	588
OY	481	ATGAG-----TTACATGTCACGTGTAACGAGCAAGAGCCTGTCACTCTCCCAAGATG	534
Db	589	ATGAGTCCAAATTACTGTGATTGTATAGCAGGAAGCCAGGATTTCTCCCTAAACTCTTG	648
OY	535	ATTATTGACACATCCAAACTGGCTCTGGAGTCCCTGTGCTTCAGTGGCAGTGGGCTC	594
Db	649	ATTATTAGACATCCAACTGGCTCTGTGAAATCCAGTCCGCTTCAGTGGCAGTGGGCTC	708
OY	595	GGGAGCTCTTATTCTCTCAATTCAGACAGCAATGAGGCTGTAGATGCTGCCACTTATTAC	654
Db	709	GGGAGCTCTTACTCTCTCAATTCAGATTTGGCAATGAGGCTGAAAGATGTTGCCACTTATTAC	768
OY	655	TGCCATCAGCGAGTAGTAGTACCCTG-----TCACGTTCCGCTGCTGGAGACACAGTTGAA	708
Db	769	TGCCACAGCGGTAGTAGTAGTACACGACGCAATTTACGTTCCGCTGCTGGAGCAAAAGTTGAA	828
OY	709	ATAAAGCG 717	
Db	829	ATAAAGCG 837	

RESULT 10

US-08-553-97A--25
 ; Sequence 25, Application US/08553497A
 ; Patent No. 5844093
 ; GENERAL INFORMATION:
 ; APPLICANT: KETTLERBOROUGH, C. A.
 ; APPLICANT: BENDIG, MARY M.
 ; APPLICANT: ANSELL, KEITH H.
 ; APPLICANT: GUSSON, DETLEF
 ; APPLICANT: ADAM, JAUDE
 ; APPLICANT: MITJANS, FRANCESCA
 ; APPLICANT: ROSELT, ELISABET
 ; APPLICANT: BLASCO, FRANCESC
 ; APPLICANT: PUJATS, JAUDE
 ; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 ; STREET: 2200 CLARENDON BLVD. SUITE 1400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: US
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/553,497A
 ; FILING DATE: 17-NOV-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/EP95/00978

FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 5 F 1 (single-chain Fv, heavy, light chain,
linker)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-08-553-497A-25

Query Match 72.7%; Score 521.6; DB 2; Length 726;
Best Local Similarity 84.4%; Pred. No. 7.2e-142;
Matches 613; Conservative 0; Mismatches 101; Indels 12; Gaps 2;

QY 1 CAGGTGAAGTTCAGAGCTGAGACCTGAACTGTGAGAGCTGGGGCTTCAGTGAAGATA 60
Db 1 CAGGTGAAGTTCAGAGCTGAGAGCTGAGAGCTGAGAGCTGGGGCTTCAGTGAAGATA 60
QY 61 TCCGCAAGAGCTTCGAGACCAATTCAGTGAATACCATGCACTGGGTGAAGCAAGAC 120
Db 61 TCCGCAAGAGCTTCGAGACCAATTCAGTGAATACCATGCACTGGGTGAAGCAAGAC 120
QY 121 CATGGAAGAGCTTGAAGTGAATGAGGTATTAATCCTAATGAGTGAATCACTAC 180
Db 121 GCTGAGCAAGGCTTGAAGTGAATGAGGTATTAATCCTAATGAGTGAATCACTAC 180
QY 181 AAGCAAGAGTTCAGAGGCAAGGCCACATTCAGTGAAGCAAGTCTCCAGCAAGCTTAC 240
Db 181 AATGAGAAATTCAGAGCAAGGCCACATTCAGTGAAGCAAGTCTCCAGCAAGCTTAC 240
QY 241 ATGAGAGTTCGAGAGCTTCAGTGAAGTTCGAGATTCGAGTCTTACTGTCAGAG-AGATAC 299
Db 241 ATGAGAGTTCGAGAGCTTCAGTGAAGTTCGAGATTCGAGTCTTACTGTCAGAG-AGATAC 299
QY 300 TAGAGTCCG-----TTGCTTACTGAGGTCCAGAGGACCAAGGTGACGCTCC 348
Db 301 TAGATTAACAGAGAGCTTGAAGTTCGAGTTCGAGGACCAAGGTGACGCTCC 360
QY 349 TCAAGTGAAGGCGGTTTCAGAGGAGTGGCTCTGCGGCTGCGGATCGAATCGAGCTC 408
Db 361 TCAAGTGAAGGCGGTTTCAGAGGAGTGGCTCTGCGGCTGCGGATCGAATCGAGCTC 420
QY 409 ACTAGTCTCCAGCAATCATCTTCGATCTTCAGAGGAGAAAGTCCACATGACTGCACT 468
Db 421 ACCAGTCTCCAGCAATCATCTTCGATCTTCAGAGGAGAAAGTCCACATGACTGCACT 480
QY 469 GGCAGCTCAAGTATTAAGTTACATGCACTGGTACCAAGCAAGAGCTGTCACTCCCCAAA 528

Db 481 GACAGCTCAAGTATTAAGTTACATGCACTGGTACCAAGCAAGAGCTGTCACTCCCCAGA 540
QY 529 AGATGATTTATGACACATCCAACTGGCTTCGAGATCCCTGCTCGCTTCAGTGGCAGT 588
Db 541 CTCCTGATTTATGACACATCCAACTGGCTTCGAGATCCCTGCTCGCTTCAGTGGCAGT 600
QY 589 GGGTCTGGAGCTCTTATTCCTTCACAAATGAGAGCAAGTGAAGGCTGTAGATGCTGCCACT 648
Db 601 GGGTCTGGAGCTCTTATTCCTTCACAAATGAGAGCAAGTGAAGGCTGTAGATGCTGCCACT 660
QY 649 TATTACTGCCATCAGCGAGTATTAACCGCTCAGCTTCGCTGCTGGGACACAGTTGGAA 708
Db 661 TATTACTGCCATCAGCGAGTATTAACCGCTCAGCTTCGCTGCTGGGACCAAGTGGAA 720
QY 709 ATAAA 714
Db 721 ATAAA 726

RESULT 11
US-08-463-163-2
Sequence 2, Application US/08463163
Patent No. 5696237
GENERAL INFORMATION:
APPLICANT: Fitzgerald, David J.
APPLICANT: Chaudhary, Vijay K.
APPLICANT: Pastan, Ira H.
APPLICANT: Waldmann, Thomas A.
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,163
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILING DATE: 22-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,722
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-12211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1797
OTHER INFORMATION: /product= "Anti-Tac(Fv)-PE40"
US-08-463-163-2

Query Match 72.2%; Score 517.4; DB 1; Length 1797;
Best Local Similarity 83.7%; Pred. No. 1.7e-140;
Matches 597; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

QY 1 CAGGTAAACCTGACAGCAGTCAAGCTGAACTGTGAGCCTGGGCTTCAGTGAAGATA 60
DB 4 CAGGTCAAGCTGACAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCTCAGTGAAGATG 63
QY 61 TCCTGCAAGACTCTTGGAACAATTCACGTGAATACCACTGACTGGGTGAAGCAGAGC 120
DB 64 TCCTGCAAGACTCTTGCTCAACCTTACTAGCTACAGATGCACTGGGTAAACAGAGG 123
QY 121 CATGAAAGAGCCTTGAGTGGATTGAGATTAATCCTTAACAATGAGTGTAACTAC 180
DB 124 CCTGACAGAGGCTTGGAATGATTTGATATTAATTCCTAGCACTGGGTATCTGAATAC 183
QY 181 AAGCAGAAAGTTCAAGGCAAGGCCACATTGACTGTAGACAAAGTCTTCACAGCAGCTAC 240
DB 184 AATCAGAAAGTTCAAGGCAAGGCCACATTGACTGTAGACAAATCTTCACAGCAGCTAC 243
QY 241 ATAGAGCTCCGAGCCTGACATCTGAGATTTCTGCACTTATTACTGTGCAAGATACT 300
DB 244 ATGCAACTGACGAGCCTGACATTTGAGGACTCTGCACTGCTATTAATCTGTGCAAGAGGG 303
QY 301 ACGGTCCCGTTTGCTTACTGGTCAAGGGAGCCAGGCTACCGTCTCTCAGGTGAGGC 360
DB 304 GGGGTC---TTTACTACTATGGGGCAAGGAAACCACTCTCACTCTCTCCGAGGCGGT 360
QY 361 GGTTCAGGCGGAGGTGCTCTGCGGTGCGGATCGGATCGGATCTCACTCACTCTCCA 420
DB 361 GGTTCAGGCGGAGGTGCTCTGCGGTGCGGATCGGATCGGATCTCACTCACTCTCCA 420
QY 421 GCAATCATGCTGATCTCTCAGAGGAGAGAGTCAACATGACCTGCACTGCACTCACT 480
DB 421 GCAATCATGCTGATCTCTCAGAGGAGAGAGTCAACATGACCTGCACTGCACTCACT 480
QY 481 ATAAAGTTACATGACTGTATCCAGCAGAAAGCTGTCACTCCCAAAAGATGATTTAT 540
DB 481 ATAAAGTTACATGACTGTATCCAGCAGAAAGCTGTCTCTCCAAAGCTGTGATTTAT 540
QY 541 GACACATCCAAACTGGCTTCTGAGATCCCTGCTTCACTGAGTGGAGTCTGGAGCC 600
DB 541 ACCACATCCAACTGGCTTCTGAGATCCCTGCTTCACTGAGTGGAGTCTGGAGCC 600
QY 601 TCTTATTTCTGCAATCAGACAGATGAGGCTGTAGATGCTGCCATTATTACTGCCAT 660
DB 601 TCTTATTTCTGCAATCAGACAGATGAGGCTGTAGATGCTGCCATTATTACTGCCAT 660
QY 661 CACGCGAGTATGACCGCTCAGCTTCGCTGCTGGGCAACAGTTGGAATATAA 713
DB 661 CAAAGAGTATTAACCACTCAGCTTCGCTTCTGGGCAACAGTGGAGCTCAA 713

RESULT 12
US-08-279-772A-7
Sequence 7, Application US/08279772A
Patent No. 6080560

GENERAL INFORMATION:
APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: PO Box 2113

CITY: Madison
STATE: WI
COUNTRY: United States of America
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9097-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..719

US-08-279-772A-7

Query Match 71.9%; Score 515.8; DB 3; Length 719;
Best Local Similarity 83.6%; Pred. No. 3.5e-140;
Matches 596; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 1 CAGGTAAACCTGACAGCAGTCAAGCCTGAACTGTGAGCCTGGGCTTCAGTGAAGATA 60
DB 7 CAGGTCAAGCTGACAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCTCAGTGAAGATG 66
QY 61 TCCTGCAAGACTCTTGGAACAATTCACGTGAATACCACTGACTGGGTGAAGCAGAGC 120
DB 67 TCCTGCAAGACTCTTGCTCAACCTTACTAGCTACAGATGCACTGGGTAAACAGAGG 126
QY 121 CATGAAAGAGCCTTGAGTGGATTGAGGATTAATCCTTAACAATGAGTGTAACTAC 180
DB 127 CCTGACAGAGGCTTGGAATGATTTGATTAATTAATTCCTAGCACTGGGTATCTGAATAC 186
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DB 187 AATCAGAAAGTTCAAGGCAAGGCCACATTGACTGTAGACAAATCTTCACAGCAGCTAC 246
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DB 247 ATGCAACTGAGCAGCCTGACATTTGAGAGCTCTGCACTTATTAATCTGTCAAGAGGGGG 306
QY 301 ACGGTCCCGTTTGCTTACTAGGGTCCAAAGGAGACAGGCTCACCGTCTCTCAGGTGAGGC 360
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Qy 661 CAGGAGATGATTACCGCTGACGTTGGTGTGGAGACAGTGGAAATAA 713
Db 664 CAAGAGTACTTACCACTACGTTCCGTTCTGGACCAAGCTGAGCTCA 716

RESULT 13
US-08-902-486-1d
Sequence 10, Application US/08902486
Patent No. 6140075
GENERAL INFORMATION:
APPLICANT: Russel, David R.
APPLICANT: Fuller, James T.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSES: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,486
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 670513.90261
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..719
NAME/KEY: CDS
LOCATION: 1..720
US-08-902-486-10

Query Match 71.9%; Score 515.8; DB 3; Length 720;
Best Local Similarity 83.6%; Pred. No. 3.5e-140;
Matches 596; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

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RESULT 14
US-08-553-497A-27
Sequence 27, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSLOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIJATLS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530

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QY 712 AAACGG 717
Db 799 AAACGG 804

Search completed: February 18, 2005, 23:56:46
Job time : 150.31 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 22:26:05 : Search time 464.472 Seconds
(without alignments)
9123.970 Million cell updates/sec

Title: US-10-075-947A-1

Perfect score: 717
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	715	99.7	717	15 US-10-075-947A-1	Sequence 1, Appl1
3	715	99.7	1176	15 US-10-075-947A-3	Sequence 3, Appl1
4	593.4	82.8	717	9 US-09-808-037-5	Sequence 5, Appl1
5	593.4	82.8	717	14 US-10-162-889-5	Sequence 5, Appl1
6	593.4	82.8	717	17 US-10-184-788-5	Sequence 5, Appl1
7	593.4	82.8	717	17 US-10-618-856-5	Sequence 5, Appl1
8	574	80.1	726	15 US-10-259-087A-19	Sequence 19, Appl1
9	574	80.1	726	18 US-10-689-006-19	Sequence 19, Appl1
10	561.4	78.3	786	18 US-10-689-006-19	Sequence 23, Appl1
11	553.2	77.2	726	15 US-10-259-087A-17	Sequence 17, Appl1

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	527.8	73.6	720	9	US-09-976-787-30	Sequence 30, Appl1																													
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ALIGNMENTS

RESULT 1
US-08-940-544-3
Sequence 3, Application US/08940544B
Publication No. US20020018783A1
GENERAL INFORMATION:
APPLICANT: SADRILAIN, MICHEL
APPLICANT: CHEUNG, NAI-KONG V.
APPLICANT: KRAUSE, ANA
APPLICANT: GUO, HONG-FEN
TITLE OF INVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: MSK.P-035-US
CURRENT FILING DATE: 1997-09-30
EARLIER APPLICATION NUMBER: PCT/US97/04427
EARLIER FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 717
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: SP11-bcfv
NAME/KEY: unsure
LOCATION: (37)
FEATURE:
NAME/KEY: unsure
LOCATION: (79)
US-08-940-544-3
Query Match 99.7%
Best Local Similarity 100.0%
Score 715; DB 8; Length 717;
Pred. No. 5.9e-228;

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; SOFTWARE:Patentlin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: SP11-bcFv
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (37)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (79)
US-10-075-947A-1

Query Match      99.7%; Score 715; DB 15; Length 717;
Best Local Similarity 100.0%; Pred. No. 5,9e-228;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CAGGTGAACCTGCAGCAGCTCAGACCTGGAACCTGGTGNACCTGGGGCTTCACTGTAAGATA 60
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; Publication No. US20030147808A1
; GENERAL INFORMATION:

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Db 601 ACCCTTATCTCTCAATCAGAGATGAGAGGCTGATGATGCTGACCTTATTAATGTCG 660
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|
|
Qy 658 CATCAGCGAGATGATACCGGCTCAGCTGCTGCTGCTGAGACACAGTTGAAATPAAA 714
|
|
|
Db 661 CATCAGCGAGATGATACCGGCTCAGCTGCTGCTGCTGAGAGGGGGCCAAAGCTGAAATPAAA 717
|
|
|

RESULT 5

US-10-162-889-5
; Sequence 5, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON-28
; CURRENT APPLICATION NUMBER: US/10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-162-889-5

Query Match 82.8%; Score 593.4; DB 14; Length 717;
Best Local Similarity 90.1%; Pred. No. 2.6e-187;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

Qy 1 CAGGTGAATCTGACGAGTCAAGACCTGAACTGGTGAAGCTGGGGCTGCTAGGAGATATA 60
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Db 1 CAGGTGAATCTGACGAGTCAAGACCTGAACTGGTGAAGCTGGGGCTGCTAGGAGATATA 60
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Qy 61 TCCTGCAAGACTTCTGAGAACCAATTGCACTGAATACCAATGCACTGGGTGAAGCAGAGC 120
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|
Db 61 TCCTGCAAGAGGTTCTGCTCAATCACTGATTAATCTATGCACTGGGTGAAGCAGAGT 120
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Qy 121 CATGGAAGAGCTTGAAGTGAATGAGGATTAATCTTAACAATGGTGGTACTAATAC 180
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|
|
Db 121 CATGGAAGAGCTTGAAGTGAATGAGGATTAATCTTAACAATGGTGGTACTAATAC 180
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Qy 181 AAGAGAGATTCAGAGGCAAGGCAACATGATCTGTAACAAGTCTCAGACAGAGCCTAC 240
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Db 181 AAGAGAGATTCAGAGGCAAGGCAACATGATCTGTAACAAGTCTCAGACAGAGCCTAT 240
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Qy 241 ATGAGAGCTCCGAGAGCTGAGATCTGAGATTTCTGCACTTAATCTGCAAGA--GAT 297
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Db 241 ATGAGAGCTCCGAGAGCTGACATCTGAGATGCTGCCATCTAATTAATCTGCAAGAGGAGCT 300
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|
Qy 298 ACTAGAGTCCGAGTCTGATGAGGTCAGAGGAGCCAGGTCACCGTCTCTCAGAGTGA 357
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Db 301 ACTAGAGTCTGATGATGATGAGGTCAGAGGAGCCAGGTCACCGTCTCTCAGAGTGA 360
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|
|
Qy 358 GCGGTTCAAGGCGAGGAGGCTCTGCGGTCGAGATCGGATCGAGTCACTGAGTCT 417
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|
|
Db 361 GCGGTTCAAGGCGAGGAGGCTCTGCGGTCGAGATCGGATCGAGTCACTGAGTCT 420
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Qy 418 CCAGCATCATGCTCTGATCTCAGGGGAGAGGATCCATGACCTGACATGCGAGTCA 477
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|
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Db 421 CCAGCATCATGCTCTGATCTCAGGGGAGAGGATCCATGACCTGACATGCGAGTCA 480
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|
|
Qy 478 AGTAAAGTAAATGATGATGCTGATCCAGAGAGGCTGTCACCTCCCAAAAGATGATT 537
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|
|
Db 481 AGTAAAGTAAATGATGATGCTGATCCAGAGAGGCTGTCACCTCCCAAAAGATGATT 540
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|
|
Qy 538 TATGACATCATGCTCTGATCTCAGGGGAGAGGATCCATGACCTGACATGCGAGTCA 597
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|
|
Db 541 TATGACATCATGCTCTGATCTCAGGGGAGAGGATCCATGACCTGACATGCGAGTCA 600
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Qy 598 ACCCTTATCTCTCAATCAGAGATGAGAGGCTGATGATGCTGACCTTATTAATGTCG 657
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|
|
Db 601 ACCCTTATCTCTCAATCAGAGATGAGAGGCTGATGATGCTGACCTTATTAATGTCG 660
|
|
|
Qy 658 CATCAGCGAGATGATACCGGCTCAGCTGCTGCTGCTGAGACACAGTTGAAATPAAA 714
|
|
|
Db 661 CATCAGCGAGATGATACCGGCTCAGCTGCTGCTGCTGAGAGGGGGCCAAAGCTGAAATPAAA 717
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|
|

RESULT 6

US-10-384-788-5
; Sequence 5, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON-2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-384-788-5

Query Match 82.8%; Score 593.4; DB 17; Length 717;
Best Local Similarity 90.1%; Pred. No. 2.6e-187;
Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Oy 1 CAGGTGAAGCTGACAGAGCTGAGACCTGAACTGTGAGAGCCTGGGGCTTCACTGTAAGATA 60
Db 1 CAGGTGAAGCTGACAGAGCTGAGAGCTGAGAGCCTGGGGCTTCACTGTAAGATA 60
Oy 61 TCTGTGAAGCTTCTGAGAACAAATTCACTGAAATACCAATGACACTGGGTGAGAGAGC 120
Db 61 TCTGTGAAGCTTCTGAGAACAAATTCACTGAAATACCAATGACACTGGGTGAGAGAGT 120
Oy 121 CATGGAAGAGCTTGAAGTGAATGAGATTTAACTCTAACTAATGAGTACTTAATAC 180
Db 121 CATGGAAGAGCTTGAAGTGAATGAGATTTAACTCTAACTAATGAGTACTTAATAC 180
Oy 181 AAGCAGAAGTTCAAGGGCAAGGCCACATTTGACTGAGCAAGCTCTCCAGACAGAGCTAC 240
Db 181 AAGCAGAAGTTCAAGGGCAAGGCCACATTTGACTGAGCAAGCTCTCCAGACAGAGCTAT 240
Oy 241 ATGAGACTCCGAGCTTGAATCATCTGAGAGATTTCTGAGTCTAATTAATCTGTCAGAGA--GAT 297
Db 241 ATGAGACTCCGAGCTTGAATCATCTGAGAGATTTCTGAGTCTAATTAATCTGTCAGAGA--GAT 297
Oy 298 ACTAGGTCCTGGTTGCTTACCTGGGTCCAGGGGACAGAGTCAAGCTCTCCAGAGTGA 357
Db 298 ACTAGGTCCTGGTTGCTTACCTGGGTCCAGGGGACAGAGTCAAGCTCTCCAGAGTGA 357
Oy 301 ACTATGCTTACTTGAATCTGAGTCAAGGGGCAAGTCAAGCTCTCCAGAGTGA 360
Db 301 ACTATGCTTACTTGAATCTGAGTCAAGGGGCAAGTCAAGCTCTCCAGAGTGA 360
Oy 358 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 417
Db 358 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 417
Oy 361 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 420
Db 361 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 420
Oy 418 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 477
Db 418 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 477
Oy 421 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 480
Db 421 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 480
Oy 478 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 537
Db 478 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 537
Oy 481 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 540
Db 481 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 540
Oy 538 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 597
Db 538 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 597
Oy 541 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 600
Db 541 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 600
Oy 598 ACTCTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 657
Db 598 ACTCTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 657
Oy 601 ACCTTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 660
Db 601 ACCTTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 660
Oy 658 CATCAGCGAGTATGTTACCGCTCACGTTCCGCTGCTGGGACACAGTTGAAATATAA 714
Db 658 CATCAGCGAGTATGTTACCGCTCACGTTCCGCTGCTGGGACACAGTTGAAATATAA 714

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RESULT 7

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US-10-618-856-5
; Sequence 5, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: SOLOMON=2A
; CURRENT APPLICATION NUMBER: US/10/618, 856
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473, 653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152, 417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)

```

US-10-618-856-5

Query Match 82.8%; Score 593.4; DB 17; Length 717;
 Best Local Similarity 90.1%; Pred. No. 2.6e-187;
 Matches 646; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

```

Oy 1 CAGGTGAAGCTGACAGAGCTGAGACCTGAACTGTGAGAGCCTGGGGCTTCACTGTAAGATA 60
Db 1 CAGGTGAAGCTGACAGAGCTGAGAGCTGAGAGCCTGGGGCTTCACTGTAAGATA 60
Oy 61 TCTGTGAAGCTTCTGAGAACAAATTCACTGAAATACCAATGACACTGGGTGAGAGAGC 120
Db 61 TCTGTGAAGCTTCTGAGAACAAATTCACTGAAATACCAATGACACTGGGTGAGAGAGT 120
Oy 121 CATGGAAGAGCTTGAAGTGAATGAGATTTAACTCTAACTAATGAGTACTTAATAC 180
Db 121 CATGGAAGAGCTTGAAGTGAATGAGATTTAACTCTAACTAATGAGTACTTAATAC 180
Oy 181 AAGCAGAAGTTCAAGGGCAAGGCCACATTTGACTGAGCAAGCTCTCCAGACAGAGCTAC 240
Db 181 AAGCAGAAGTTCAAGGGCAAGGCCACATTTGACTGAGCAAGCTCTCCAGACAGAGCTAT 240
Oy 241 ATGAGACTCCGAGCTTGAATCATCTGAGAGATTTCTGAGTCTAATTAATCTGTCAGAGA--GAT 297
Db 241 ATGAGACTCCGAGCTTGAATCATCTGAGAGATTTCTGAGTCTAATTAATCTGTCAGAGA--GAT 297
Oy 298 ACTAGGTCCTGGTTGCTTACCTGGGTCCAGGGGACAGAGTCAAGCTCTCCAGAGTGA 357
Db 298 ACTAGGTCCTGGTTGCTTACCTGGGTCCAGGGGACAGAGTCAAGCTCTCCAGAGTGA 357
Oy 301 ACTATGCTTACTTGAATCTGAGTCAAGGGGCAAGTCAAGCTCTCCAGAGTGA 360
Db 301 ACTATGCTTACTTGAATCTGAGTCAAGGGGCAAGTCAAGCTCTCCAGAGTGA 360
Oy 358 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 417
Db 358 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 417
Oy 361 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 420
Db 361 GCGGTTTCAGGCGAGAGTGGCTCTGGCGGTGGCGAGTGGACATGAGAGCTCACTAGTCT 420
Oy 418 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 477
Db 418 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 477
Oy 421 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 480
Db 421 CAGCAATCATGCTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGCTCA 480
Oy 478 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 537
Db 478 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 537
Oy 481 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 540
Db 481 AGTAAGTTAATGCACTGCTGATCTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGAGT 540
Oy 538 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 597
Db 538 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 597
Oy 541 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 600
Db 541 TATGACATCAACAACTGGCTTCTGAGAGTCCCTGCTCAGTGGAGTGGGTCTGGG 600
Oy 598 ACTCTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 657
Db 598 ACTCTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 657
Oy 601 ACCTTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 660
Db 601 ACCTTTATTTCTCTCAATCAGCAGATGAGAGGCTGTAGATGCTGCCACTTATTACTGC 660
Oy 658 CATCAGCGAGTATGTTACCGCTCACGTTCCGCTGCTGGGACACAGTTGAAATATAA 714
Db 658 CATCAGCGAGTATGTTACCGCTCACGTTCCGCTGCTGGGACACAGTTGAAATATAA 714

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RESULT 8

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US-10-259-087A-19
; Sequence 19, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259, 087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 726

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
;
; NAME/KEY: CDS
; LOCATION: (1)..(726)
; OTHER INFORMATION:
US-10-259-087A-19
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Query Match      80.1%; Score 574; DB 15; Length 726;
Best Local Similarity 88.2%; Pred. No. 7.9e-181;
Matches 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;
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QY 1 CAGGTGAAGCTGACGAGCTGAGACCTGAACTGGTGAAGCTGGGGCTTCAGTGAAGATA 60
DB 7 CAGGTCAAGCTGACGAGCTGAGACCTGAACTGGTGAAGCTGGGGCTTCAGTGAAGATA 66
QY 61 TCCTGCAAGACTTCTGGANACAAATTCATGTAATACATGCACTGGGTGAAGCAGAGC 120
DB 67 TCCTGCAAGAGCTTCTGGATACACATTCATGTAATGCACTGGGTGAAGCAGAGC 126
QY 121 CATGAAAGAGCTTGAAGTGAATGAGTATTATCTTAACAATGSGTACTAATAC 180
DB 127 CCTGGCAGAGGCTTGAAGTGAATGAGTATTATCTTAACAATGAGTGAATAC 186
QY 181 AAGCAAGATTCAAGGCGAAGGCCACATGACTGTACAAAGTCTTCAGACAGCCTAC 240
DB 187 AATGAAGATTCAAGGCGAAGGCCACATGACTGTACAAAGTCTTCAGACAGCCTAC 246
QY 241 ATGAGCTCCGACGCTGACATCTGAGATTCGACATCTATTACTGTGCAAGA--GAT 297
DB 247 ATGAGCTCCGACGCTGACATCTGAGATTCGACATCTATTACTGTGCAAGTTGGT 306
QY 298 ACTACGCTCCGTTTCTTACTGTGGTCCAAAGGACACAGCTCACGCTCTCTCAGGTGA 357
DB 307 AACTACGCTGCTTGGACTACTGTGGGCGCAAGGACACAGCTCACGCTCTCTCAGGTGA 366
QY 358 GGGGCTTCAGGCGGAGGTGGCTCGGGGTGGCGGATCGGACATCGAGCTCACTCACT 417
DB 367 GGGGCTTCAGGCGGAGGTGGCTCGGGGTGGCGGATCGGACATCGAGCTCACTCACT 426
QY 418 CCAACAATCATATGTCATCTCCAGGGAGAGGTCACTGACCTGCACTGAGTGCAGCTCA 477
DB 427 CCAACAATCATATGTCATCTCCAGGGAGAGGTCACTGACCTGCACTGAGTGCAGCTCA 486
QY 478 AGTATAAGTTACATGCACTGTGTACAGAGAAAGCTGTCACTCTCCCAAAAGTGAAT 537
DB 487 AGTATAAGTTACATGCACTGTGTGTCCAGAGAAAGCTGTCTCTCCCAAAAGTGAAT 546
QY 538 TATGACATCATCAACCTGGCTTCTGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
DB 547 TATGACATCATCAACCTGGCTTCTGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
QY 598 ACTCTTATTTCTCAACAATCAGACAGATGAGGCTGTAGATGCTGCACTTATTATTCG 657
DB 607 ACTCTTATTTCTCAACAATCAGACAGATGAGGCTGTAGATGCTGCACTTATTATTCG 666
QY 658 CATCAGGAGTATGATACCGGCTCAAGTTCGCTGCTGAGACACAGTTGGAATTAACG 717
DB 667 CAACAGTGAAGTATGATACCGCACTCAAGTTCGAGAGGGGAGCAACAGCTGGAATTAACG 726
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RESULT 9
US-10-689-006-19
; Sequence 19, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
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; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
; NAME/KEY: CDS
; LOCATION: (1)..(726)
US-10-689-006-19
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Query Match      80.1%; Score 574; DB 18; Length 726;
Best Local Similarity 88.2%; Pred. No. 7.9e-181;
Matches 635; Conservative 0; Mismatches 82; Indels 3; Gaps 1;
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QY 1 CAGGTGAAGCTGACGAGCTGAGACCTGAACTGGTGAAGCTGGGGCTTCAGTGAAGATA 60
DB 7 CAGGTCAAGCTGACGAGCTGAGACCTGAACTGGTGAAGCTGGGGCTTCAGTGAAGATA 66
QY 61 TCCTGCAAGACTTCTGGANACAAATTCATGTAATACATGCACTGGGTGAAGCAGAGC 120
DB 67 TCCTGCAAGAGCTTCTGGATACACATTCATGTAATGCACTGGGTGAAGCAGAGC 126
QY 121 CATGAAAGAGCTTGAAGTGAATGAGTATTATCTTAACAATGSGTACTAATAC 180
DB 127 CCTGGCAGAGGCTTGAAGTGAATGAGTATTATCTTAACAATGAGTGAATAC 186
QY 181 AAGCAAGATTCAAGGCGAAGGCCACATGACTGTACAAAGTCTTCAGACAGCCTAC 240
DB 187 AATGAAGATTCAAGGCGAAGGCCACATGACTGTACAAAGTCTTCAGACAGCCTAC 246
QY 241 ATGAGCTCCGACGCTGACATCTGAGATTCGACATCTATTACTGTGCAAGA---GAT 297
DB 247 ATGAGCTCCGACGCTGACATCTGAGATTCGACATCTATTACTGTGCAAGTTGGT 306
QY 298 ACTACGCTCCGTTTCTTACTGTGGTCCAAAGGACACAGCTCACGCTCTCTCAGGTGA 357
DB 307 AACTACGCTGCTTGGACTACTGTGGGCGCAAGGACACAGCTCACGCTCTCTCAGGTGA 366
QY 358 GGGGCTTCAGGCGGAGGTGGCTCGGGGTGGCGGATCGGACATCGAGCTCACTCACT 417
DB 367 GGGGCTTCAGGCGGAGGTGGCTCGGGGTGGCGGATCGGACATCGAGCTCACTCACT 426
QY 418 CCAACAATCATATGTCATCTCCAGGGAGAGGTCACTGACCTGCACTGAGTGCAGCTCA 477
DB 427 CCAACAATCATATGTCATCTCCAGGGAGAGGTCACTGACCTGCACTGAGTGCAGCTCA 486
QY 478 AGTATAAGTTACATGCACTGTGTACAGAGAAAGCTGTCACTCTCCCAAAAGTGAAT 537
DB 487 AGTATAAGTTACATGCACTGTGTGTCCAGAGAAAGCTGTCTCTCCCAAAAGTGAAT 546
QY 538 TATGACATCATCAACCTGGCTTCTGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
DB 547 TATGACATCATCAACCTGGCTTCTGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
QY 598 ACTCTTATTTCTCAACAATCAGACAGATGAGGCTGTAGATGCTGCACTTATTATTCG 657
DB 607 ACTCTTATTTCTCAACAATCAGACAGATGAGGCTGTAGATGCTGCACTTATTATTCG 666
QY 658 CATCAGGAGTATGATACCGGCTCAAGTTCGCTGCTGAGACACAGTTGGAATTAACG 717
DB 667 CAACAGTGAAGTATGATACCGCACTCAAGTTCGAGAGGGGAGCAACAGCTGGAATTAACG 726
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RESULT 10

US-10-689-006-23
Sequence 23, Application US/10689006
Publication No. US20040191249A1
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Mernaugh, Raymond
TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
FILE REFERENCE: 1242/72
CURRENT APPLICATION NUMBER: US/10/689,006
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US 09/914,605
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 786
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: nucleic acid encoding scFv antibody 10A
FEATURE: 1
NAME/KEY: CDS
LOCATION: (1)..(786)
US-10-689-006-23

Db 427 CCAACAAACGATGGTCATCTCCAGAGAGAGATGACCAATCACTCCGTCGACAGCTCA 486
Qy 478 AGTATAGTATCATGACCTGTGTACACAGACAGCCTTCTACCTCCCAAAAGATGATT 537
Db 487 AGGTATAGTATCATGACCTGTGTGTCCACAGAAAGTCAAGCAGCCTCCCAAAACCTTGATT 546
Qy 538 TATGACATCATCAAACTGGCTTGTGAGTCCCTGCTGCTTCACTGAGTGGGCTGGG 597
Db 547 TATGACATCATCAAGCTGGCTTGTGAGTCCCAAGATGCTTCACTGAGTGGGCTGGG 606
Qy 598 ACCCTTATTTCTCTACAAATCAGCAGCATGAGAGCTGTAGATGCTGCACCTTATTCTGC 657
Db 607 ACCCTTATTTCTCTCAAAATCAGCTCCATGAGGCTGAAGTGTCTTATTATTACTGT 666
Qy 658 CATGACGAGAGTATGATCCCGCTCAAGTTGGTGTGGGACACAGTTGGAATPAAACGG 717
Db 667 CTGACAGAGAGTATGATCCCGTACACGTTTGGAGCTGGCAACAAGCTGGAATCAACGG 726

RESULT 12

US-10-689-006-17
; Sequence 17, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689, 006
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(726)
US-10-689-006-17

Query Match 77.2%; Score 553.2; DB 18; Length 726;

Best Local Similarity 86.4%; Pred. No. 7.1e-174; Indels 3; Gaps 1;

Matches 622; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

Qy 1 CAGGTGAAGTGCAGAGTGCAGAGCTGAACCTGCTGAGAGCTGGGCTTCACTGTAAGATA 60
Db 7 CAGGTGAAGTGCAGAGTGCAGAGCTGAGCTGTGTGTGATGCTGGGCTTCACTGTAAGATA 66
Qy 61 TCTTCGAAGACTTTTGGANCAATTTCACTGAATACCATGCACTGGGTGAAGCAGAGC 120
Db 67 TCTTCGAAGAGCTTCTGCTACACATTCATGCACTGATGCACTGGGTGAAGCAGAGC 126
Qy 121 CATGGAAGAGCTTGTGAGTGTGAGGTATTAATCTTAACATGTGGGTGAATCACTAC 180
Db 127 CTGGAAGAGCTTGTGAGTGTGAGGTATTAATCTTGTATGATGATTAATCACTAC 186
Qy 181 AAGCAGAAGTTCAGAGGCAAGCCATTTGACTGTAGACAAAGTCTCCAGACAGCCTAC 240
Db 187 AATCAAAAGTTCAAGGGGCAAGCCATTTGACTGTAGACAAAGTCTCCAGACAGCCTAC 246
Qy 241 ATGAGCTCCGAGCTGTACATCTGAGAGTTCTGCAAGTCTATTACTGTGC---AAGAGAT 297
Db 247 ATGAGCTCCGAGCTGTACATCTGAGAGTTCTGCAAGTCTATTACTGTGCAAGAGAGGC 306

Qy 298 ACTACGTCCTCGTTTGTCTTACTGAGGTCCAAGGACCAAGCTCAAGCTCTCTCAGGTGGA 357
Db 307 TACTATAGGCAATTTGATTTACTGAGGCAAGGGAAGTCAAGCTCAAGCTCTCTCAGGTGGA 366
Qy 358 GGGGTTTCAAGGCGAGTGGCTTGTGCGGTCGGATCGGAATGAGTCACTACAGTCT 417
Db 367 GGGGTTTCAAGGCGAGTGGCTTGTGCGGTCGGATCGGAATGAGTCACTACAGTCT 426
Qy 418 CCAAGCAATGATGTCATCTCCAGGGGGAAGGTCAACCATGACCTGCAGTGGAGCTCA 477
Db 427 CCAACCAAGTGGCTGATCTCCAGGAGAAAGTCAACCATGACCTGCAGTGGAGCTCA 486
Qy 478 AGTATAGTATCATGACCTGTGTACAGCAAGACCTGTCACTCCCAAAAGATGATT 537
Db 487 AGGTATAGTATCATGACCTGTGTGTCCAGCAAGAGTCAAGGACCTCCCAAAACCTTGATT 546
Qy 538 TATGACATCATCAAACTGGCTTGTGAGTCCCTGCTGCTTCACTGAGTGGAGTGGG 597
Db 547 TATGACATCATCAAGCTGGCTTGTGAGTCCCAAGATGCTTCACTGAGTGGAGTGGG 606
Qy 598 ACCCTTATTTCTCTCAATCAGCAGCATGAGAGCTGTAGATGCTGCACCTATTACTGC 657
Db 607 ACCCTTATTTCTCTCAATCAGCTCCATGAGGCTGAAGATGCTGCTATTATTACTGT 666
Qy 658 CATGACGAGAGTATGATCCCGCTCAAGTTGGTGTGGGACACAGTTGGAATPAAACGG 717
Db 667 CTGACAGAGAGTATGATCCCGTACACGTTTGGAGCTGGCAACAAGCTGGAATCAACGG 726

RESULT 13

US-10-408-930-4
; Sequence 4, Application US/10408930
; Publication No. US20030170820A1
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION
; FILE REFERENCE: 674537-2003.1
; CURRENT APPLICATION NUMBER: US/10/408, 930
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/AU99/00341
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 09/674,677
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: AU PP3445
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.Feature
; LOCATION: (1)..(807)
; OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4c2) scFv
US-10-408-930-4

Query Match 76.4%; Score 547.6; DB 16; Length 807;

Best Local Similarity 85.2%; Pred. No. 5.5e-172; Indels 0; Gaps 0;

Matches 610; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 2 AGGTGAAGTGCAGAGTGCAGAGCTGAACCTGCTGAGAGCTGGGCTTCACTGTAAGATA 61
Db 10 ATGTGAAGCTTCAAGAGTCAAGGCTGAGCTGTGTGAGGCTCCGGGCTCTCACTGAAGATA 69
Qy 62 CCGCAAGACTTCTGAGANCAATTTCACTGAATACCAATGCACTGGGTGAAGCAGAGCC 121
Db 70 CCGCAAGGTTCTCGGCTACATTCATGATTAATGATGATTTGGTGAAGCAGAGTC 129
Qy 122 ATGGAAGAGCTTGTGAGTGTGAGGTATTAATCTTAACATGATGTTGTTACTTAATCA 181
Db 130 ATGCAAGAGTGTGAGTGTGAGGTATTAATCTTAATCTTGTGTAATCAAACTACA 189

182 AGCAAGATTCAAGGCGCAAGCCATTGATGTAGACAGTCTCCAGCAGAGCTTACA 241
Db ACGAAGATTGAGGCGCAAGGCGCAATGATGTAGACAAATCTCCAGCAGAGCTTATT 249
Qy 242 TGAAGCTCCGAGAGCTGACATGTAGAGATTCTGAGTCTTATTACTGTGCAAGAGTACTA 301
Db 250 TGAAGCTTGGAGAGATTGACATGTAGAGATTCTGAGTCTTATTACTGTGCAAGAGTACTG 309
Qy 302 CAGTCCGCTTGTCTTACTGTGAGTCCAGGAGCAAGGTCACCGTCTCTCTCAAGTGAAGCG 361
Db 310 AGTGTCTTGTGATGTCTGTGGGCGCAAGGAGCAAGGTCACCGTCTCTCTCAAGTGAAGCG 369
Qy 362 GTTCAGCGGAGAGTGGCTCTGGCGGTGGCGAGTCCGAGATCCGAGTCACTCACTGCTCCAG 421
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Qy 422 CAATCATGTGTGATCTTCAGGAGGAGAAAGTCCACCATGACCTGCAAGTGGAGCTCAAGTA 481
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Qy 482 TAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
Db 490 TCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
Qy 542 AACAATCCAACTGGCTCTGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
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Qy 602 CTATATCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 661
Db 610 CTCACTCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 669
Qy 662 AGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
Db 670 AGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725

RESULT 14

US-10-247-488-1
Sequence 1, Application US/10247488
Publication No. US20030022244A1
GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
FILE REFERENCE: 1196336-RAMOT
CURRENT APPLICATION NUMBER: US/10/247,488
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/526,738
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 771
TYPE: DNA
ORGANISM: Humanus
US-10-247-488-1

Query Match 74.5%; Score 534.2; DB 14; Length 771;
Best Local Similarity 84.9%; Pred. No. 1.6e-167;
Matches 609; Conservative 0; Mismatches 105; Indels 3; Gaps 1;
Qy 1 CAGGTGAATCTGACAGAGCTGACAGCTGAACTGTGTGAGGCTGTGAGTGAAGTATA 60
Db 1 CAGGTGAATCTGACAGAGCTGTGGGCTGAACTGTGCAAACTGTGGGCTCTGAGTAAAGATG 60
Qy 61 TCTGTGAAGACTTCTGTGAGAACAAATTCAGTGAATACACATGCACTGGGTGAAGCAGAGC 120
Db 61 TCTGTGAAGACTTCTGTGCTACACCTTTACTAGCTACTGATGAACTGGGTAAACAGAGG 120
Qy 121 CATGAAAGAGCCTTGAAGTATGAGAGTATTAATCTTAACAATGTGTACTACTAC 180
Db 121 CCTGAGACGGGTCTGGAATGATGATGATTAATCTTACACACTGGTATTAATCAAGTAC 180

181 AAGCAAGATTCAAGGCGCAAGCCATTGATGTAGACAGTCTCCAGCAGAGCTTACA 240
Db 181 AATGAGAGTTCAAGGAGCAAGGCGCAATGATGTAGACAAATCTCCAGCAGAGCTTACT 240
Qy 241 ATGAGCTCCGAGAGCTGACATGTAGAGATTCTGAGTCTTATTACTGTGCAAGAGTACT 300
Db 241 ATGCAACTGAGCAGCTGACCAATGATGAGTCTGCAAGTCTTATTATGACAACTGGTACT 300
Qy 301 ACGTCCGCTTGTCTTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 301 TC---TTATTTTACTGTGGGCGCAAGGAGCAAGGTCACCGTCTCTCTCAAGTGAAGCG 357
Qy 361 GATTCAAGCGGAGGCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 420
Db 358 GATTCAAGCGGAGGCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 417
Qy 421 GCAATCATGTGTGATCTTCAGGAGGAGAAAGTCCACATGACCTGCAAGTGGAGCTCAAGT 480
Db 418 GCAATCATGTGTGATCTTCAGGAGGAGAAAGTCCACATGACCTGCAAGTGGAGCTCAAGT 477
Qy 481 ATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 478 GTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
Qy 541 GACAATCCAACTGGCTCTGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 538 AGCAATCCAACTGGCTCTGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
Qy 601 TCTTATCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 660
Db 598 TCTTATCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 657
Qy 661 CAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
Db 658 CAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714

RESULT 15

US-10-247-488-3
Sequence 3, Application US/10247488
Publication No. US20030022244A1
GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
FILE REFERENCE: 1196336-RAMOT
CURRENT APPLICATION NUMBER: US/10/247,488
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/526,738
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 780
TYPE: DNA
ORGANISM: Humanus
US-10-247-488-3

Query Match 74.5%; Score 534.2; DB 14; Length 780;
Best Local Similarity 84.9%; Pred. No. 1.6e-167;
Matches 609; Conservative 0; Mismatches 105; Indels 3; Gaps 1;
Qy 1 CAGGTGAATCTGACAGAGCTGACAGCTGAACTGTGTGAGGCTGTGAGTGAAGTATA 60
Db 7 CAGGTGAATCTGACAGAGCTGTGGGCTGAACTGTGCAAACTGTGGGCTCTGAGTAAAGATG 66
Qy 61 TCTGTGAAGACTTCTGTGAGAACAAATTCAGTGAATACACATGCACTGGGTGAAGCAGAGC 120
Db 67 TCTGTGAAGACTTCTGTGCTACACCTTTACTAGCTACTGATGAACTGGGTAAACAGAGG 126
Qy 121 CATGAAAGAGCCTTGAAGTATGAGAGTATTAATCTTAACAATGTGTACTACTAC 180
Db 127 CCTGAGACGGGTCTGGAATGATGATGATTAATCTTACACACTGGTATTAATCAAGTAC 186

Oy	18	AACGAGAAAGTTCAAGGGCAAGGCA	CATTGATCTGAGACAAGTCTCCAGACAGCTTAC	24.0
Dp	187	AATCAGAAAGTTCAAGGACAAAGGCC	CATTGACTGACAGCAAAATCTCCAGCAGGGCTTAC	24.6
Oy	241	ATGAGAGCTCCGACGCTGACATCT	GAGATTTCTGAGTCTATTATCTGTGACAGAGATACT	30.0
Dp	247	ATTCACACTGACGAGCCTGACCAAT	GAGTCACTCTGACAGTCTATTATTGTCACAAGTGATAC	30.6
Oy	301	ACGGATCCCGTTTACTTACTGAGG	TCCAGAGGACCAAGCTCAACGGTCTCCTCAGGTGAGAGGC	36.6
Dp	307	TC---	TTATTTTATCTACTGAGGCCAAGG	36.3
Oy	361	GGTTCAAGCGGAGGTGGCTCTG	GGGTGGGATTCGACATCGAGCTCACTCACTCTCCA	42.0
Dp	364	GGTTCAAGGCCGAGTGGCTCTG	GGCGGTGGGATTCGACATCGAGCTCACTCACTCTCCA	42.3
Oy	421	GCATCATGTCTGCATCTCTCAG	GGGAGAAAGTTCACATGACCTGACAGTGGAGCTCAAGT	48.0
Dp	424	GCATCATGTCTGCATCTCTCAG	GGGAGAAAGTTCACATGACCTGAGTGGAGCTCAAGT	48.3
Oy	481	ATAAGTTACATGCACGTGGTAC	CAAGCAAGCTCTGCACTCCCAAAAAGATGGATTTAT	54.0
Dp	484	GTAATATTACATGCACGTGGTAC	CAAGCAAGCTCTGCACTCCCAAACTCTGGATTTTCT	54.3
Oy	541	GACACATCCAAATGGCTCTG	AGATCCCTGGCTCAATGGCAAGTGGCTCTGGGAC	60.0
Dp	544	AGCACATCCAACTGGCTCTG	AGATCCCTGGCTCTGCAATGGGAGTGGGATCTGGGAC	60.3
Oy	601	TCTTATCTCTCAACATCAG	CAAGCAATGAGGCTGTGATGTGTGCACATTATTACTGTGCAT	66.0
Dp	604	TCTTATCTCTCAACATCAG	CAAGGAGGCTGTGATGTGTGCACATTATTACTGTGCAG	66.3
Oy	661	CACGCGAGTGTAAACCCGCT	CAACGTTCCGCTCTGGGACACAGTTGGAAATTTAAACGG	71.7
Dp	664	CAAGGAGTGTAAACCCATCA	AGTTCGGAAGGGGGGACCAAGCTGCAATATTAACCG	72.0

Search completed: February 19, 2005, 02:16:16
Job time : 466.472 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 20:04:30 : Search time 2571.88 Seconds
(without alignments)
10611.722 Million cell updates/sec

Title: US-10-075-947A-1

Perfect score: 1 caggtcgaaactgcagcagtc.....cacagtcgaaataaacgg 717

Sequence:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_nlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss81:*
9: gb_gss82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	437.2	61.0	872	7	CK629396 AMO-AA001
2	431.6	60.2	601	5	BQ474958 carabua4g
3	426.6	59.5	1104	7	CK629846 AM2-AA002
4	415	57.9	1419	7	CK629415 AM1-AA001
5	413.6	57.7	1339	7	CK629414 AM1-AA001
6	368.2	51.4	672	7	CK633068 AM3-AP001
7	368.2	51.4	672	7	CK633069 AM3-AP001
8	344.6	48.1	963	7	CK629843 AM2-AA002
9	344	48.0	823	7	CK632348 AM0-AA000
10	336.4	46.9	567	5	BQ328142 MR4-RT004
11	329.4	45.9	585	4	BI030095 IL0-MT035
12	316.8	44.2	476	2	BF923394 QV4-NT024
13	315.8	44.0	498	2	BF857861 QV1-FT020
14	313	43.7	488	2	BF857860 QV1-FT020
15	307.8	42.9	427	5	BQ373705 QV1-FT017
16	305.8	42.6	452	4	BI055323 RC0-GN023
17	301.8	42.1	653	5	BQ321980 MR1-CT073
18	300.2	41.9	565	2	BF801321 MR0-CT002
19	297.2	41.5	544	5	BQ310337 MR0-BT450
20	294.6	41.1	489	2	BF855522 PM2-FN021
21	293.4	40.9	413	2	BF923369 QV4-NT024
22	293	40.9	403	5	BQ375976 RC3-TN009
23	293	40.9	416	4	BI025870 IL0-MT036
24	293	40.9	419	5	BQ321312 RC0-CT047

25	293	40.9	424	5	BQ376239	BQ376239 MR4-TN010
26	293	40.9	427	2	BF752315	BF752315 RC3-BN042
27	293	40.9	437	5	BQ321307	BQ321307 RC0-CT047
28	293	40.9	439	5	BQ321297	BQ321297 QV1-CT041
29	293	40.9	445	5	BQ321751	BQ321751 MR1-CT052
30	293	40.9	448	5	BQ321310	BQ321310 RC0-CT047
31	293	40.9	449	5	BQ321309	BQ321309 RC0-CT047
32	293	40.9	449	5	BQ372280	BQ372280 RC0-CT018
33	293	40.9	454	2	BF836107	BF836107 QV4-HT101
34	293	40.9	455	4	BI030044	BI030044 IL0-MT034
35	293	40.9	457	5	BQ337457	BQ337457 IL0-MT035
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42	293	40.9	473	5	BQ321749	BQ321749 MR1-CT052
43	292	40.7	407	5	BQ328151	BQ328151 MR4-RT004
44	292	40.7	455	4	BI030093	BI030093 IL0-MT035
45	292	40.7	458	4	BI063593	BI063593 IL3-UT011

ALIGNMENTS

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LOCUS
DEFINITION AMO-AA0013-110902-011-H03-AA0013 Apis mellifera cDNA, mRNA
ACCESSION CK629396
VERSION CK629396
KEYWORDS CK629396.1 GI:45753871
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea; Apidae; Apis
1 (bases 1 to 872)
Munes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., pinheiro,D.G.,
Mata,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,B., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.B., Biondi,M.W.G., Espereifico,E.M.,
Espindola,F.S., Peco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A., Jr.
Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonj@usp.br
This sequence was derived from the PAPSP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.
Location/Qualifiers
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TITLE JOURNAL
COMMENT
ORIGIN
Query Match 61.0%; Score 437.2; DB 7; Length 872;

Best Local Similarity 81.8%; Pred. No. 7.4e-118;
Matches 529; Conservative 0; Mismatches 111; Indels 7; Gaps 2;

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Db 752 GCTACATCTTCACAGATTATGATATGACCTGGGAGGAGCAGACCCCTGAAACAGGACTTG 693
QY 137 AGTGAATTTGGAGGATTAATCTTAACAATGGTGTACTTAATCAACAGCAGAAGTTCAAG 196
Db 692 AGTGAATTTGGAGGATTTT-TCCTGGAGAGGGAGTACTGAATACATGAGAAAGTTCAAG 634
QY 197 GCAAGGCCACATTTACTGTAGACACAAGTCTTCACAGCAGCCTACATGAGTCCGACGCC 256
Db 633 GCAAGGCCACACGTAGTGTAGACACAAGTCTTCACAGCAGCCTATATGAGTCACTAGCC 574
QY 257 TGACATCTGAGGATTTCTGACGTCTATTACTGTGCAAGAG-----ATATACGGTCCCTG 310
Db 573 TGACATCTGAGGATCTGCTGTCTATTCTGTCTAGAGGAGGACTACTATATGAGCGCTACT 514
QY 311 TTGCTTACTGGGATCCAGAGGACCAAGGTCACCGCTCTCAGAGTGAAGGGGTTCAAGCG 370
Db 513 TTGACTTTGGAGGACCAAGGACCAAGGTCACCGCTCTCAGAGTGAAGCGGTTCAAGCG 454
QY 371 GAGGTGCTCTGGCGGTGGCGGATCGACATCGAGCTCACTAGTCTTCAGCAATCATGT 430
Db 453 GAGGTGCTCTGGCGGTGGCGGATCTGACATTTAGCTCACCGAGTCTTCAGCAATCATGT 394
QY 431 CTGATATCTCCAGGGGAAAGAGTCAACATGACCTGCAAGTGGAGCTCAAGTAAATTACA 490
Db 393 CTGATATCTCCAGGGGAAAGAGTCAACATGACCTGCAAGTGGAGCTCAAGTAAATTACA 334
QY 491 TGCACTGTGATCCAGCAGAGGCTGTGACCTCCCCCAAAAGATGGATTATGACACATCA 550
Db 333 TAAATTTGTATCCACAGAGGCTGTGATCTTCCCAACATCTCTGATTTATGACACATCA 274
QY 551 AACTGCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGGTCTGGAGCTCTTATTTCTC 610
Db 273 AACTGCTTCTGAGTCCCTTTCCTTTCGCTTCAAGTGGAGTGGTCTGGAGCTCTTATTTCTC 214
QY 611 TCACATTCAGCAGATGAGGCTGTAGATGCTGCCATTATTTACTGCTCATCAGGAGTAA 670
Db 213 TCACATTCAGCAGATGAGGCTGTAGATGCTGCCATTATTTACTGCTCAGAGTGGAGT 154
QY 671 GTTACCCGCTCAGGTTGGTGGTGGGACACAGTTGAAATTAACCG 717
Db 153 GTTATCCGTACAGCTTGGAGGGGGACCAAGCTTGAGCTGAACCG 107
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RESULT 2
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LOCUS Carabus9412.b Carabus granulatus cDNA Carabus granulatus cDNA clone
DEFINITION Carabus9412 5', mRNA sequence.
ACCESSION BO474958
VERSION BO474958.1 GI:25957232
KEYWORDS EST.
SOURCE Carabus granulatus
ORGANISM Carabus granulatus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae; Carabini;
Carabina; Carabus; Carabus.
1 (bases 1 to 601)
Theodorides,K., de Riva,A., Gomez-Zurita,J., Foister,P.G. and
Vogler,A.P.
Comparison of EST libraries from seven beetle species: towards a
framework for phylogenomics of the Coleoptera
Insect Mol. Biol. 11 (5), 467-475 (2003)
JOURNAL MEDLINE
PUBMED 22217875
12230545
Contact: Foister PG
Vogler, Entomology
The Natural History Museum
Cromwell Road, London, SW7 5BD

FEATURES
source
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/clone_1b="Carabus granulatus cDNA"
/note="Vector: pUC18"

ORIGIN
Query Match 60.2%; Score 431.6; DB 5; Length 601;
Best Local Similarity 84.1%; Pred. No. 3e-116;
Matches 501; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

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Db 600 AGGACTTGATGATGATTTGATGATTTTCTTGAGAGGGAGTACTGAATACATGAGAGA 541
QY 188 AGTTCAAGGCAAGGCCACATTGACTGTAGACAAAGTCTTCACAGCAGCCTATATGAGC 247
Db 540 AGTTCAAGGCAAGGCCACACATGATGTAGACAAAGTCTTCACAGCAGCCTATATGAGC 481
QY 248 TCCGACGCTGACATCTGAGGATTTCTGACGTCTATTACTGTGCAAGAG-----ATACTA 301
Db 480 TCACTAGGCTGACATCTGAGGATCTGCTGTCTATTCTGTCTAGAGGGAGTACTATA 421
QY 302 CGGTCCGTTTGCTTACTGAGGATTCAGAGGACCAAGGTCACCGTCTCTCTAGTGAAGCG 361
Db 420 GCGCTACTTGTGCTTGTGGGGCCAAAGGACCAAGGTCACCGTCTCTCTATGTGAGAGCG 361
QY 362 GTTCAGGCGGAGGTGCTCTGCGCGTGGGAGTCCGACATGAGCTCACTAGTCCGAG 421
Db 360 GTTCAGGCGGAGGTGCTCTGCGCGTGGGAGTCCGACATGAGCTCACTAGTCCGAG 301
QY 422 CAATCATGCTGATCTCCAGGGGAGAGGTCACATGACCTGCAAGTGGAGCTCAAGTA 481
Db 300 CAATCATGCTGATCTCCAGGGGAGAGGTCACATGAGCTGCAAGTGGAGCTCAAGTA 241
QY 482 TAAATTAATGACATGCTGTACAGAGAGCTGTGACCTCCCCAAAGATGGATTTATG 541
Db 240 TAAATTAATTAATTTGTATGATCAAGAGAGCTGTGACCTCCCCAAAGATGGATTTATG 181
QY 542 ACAATCCAAACCTGGTCTGAGAGTCCCTGCTGCTTCAAGTGGAGTGGTCTGGAGCT 601
Db 180 ACAATCCAAACCTGGTCTGAGAGTCCCTTTCGCTTCAAGTGGAGTGGTCTGGAGCT 121
QY 602 CTATTCTCTCAACATCAGCAGATGAGGCTGTAGATCTGCCATTATTACTGCCATC 661
Db 120 CTATTCTCTCAACATCAGCAGATGAGGCTGTAGATCTGCCATTATTACTGCCAG 61
QY 662 AGCGAGTATTAACCCGCTCAGCTTGGTGGTGGGACACAGTTGAAATTAACCG 717
Db 60 AGTGAAGTGTATTCGTACAGTTCGAGGGGGACCAAGCTTGAGCTGAACCG 5
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RESULT 3
CK629846/c 1104 bp mRNA linear EST 26-MAR-2004
LOCUS CK629846
DEFINITION AM2-AA0023-091202-021-F02 AA0023 Apis mellifera cDNA, mRNA
sequence.
ACCESSION CK629846
VERSION CK629846.1 GI:45754321
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apoidea; Apis.
1 (bases 1 to 1104)
Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monezi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,

Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Espindola, F.S., Peco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, M.A. Jr.

TITLE Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome

JOURNAL Unpublished (2004)

CONTACT: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory

Departament of Genetics, FMRP/USP, FUNDHERP

Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639309

Fax: +55 16 39639309

Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program
High quality sequence start: 64
High quality sequence stop: 594.

Location/Qualifiers

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1..1104
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_id="AA0023"
/note="Organ: whole body"
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ORIGIN

Query Match 59.5%; Score 426.6; DB 7; Length 1104;
Best Local Similarity 81.2%; Pred. No. 1.1e-114;
Matches 534; Conservative 0; Mismatches 115; Indels 9; Gaps 3;

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OY 68 AGACTTTGGAACAATTCCTGAATACCATGATGCGGTGAAGAGCCATGGA-126
DB 747 AGCGTTCTTGCTCATCTTCAAGATTATGATATAGACTGTTGAGGACGCGTGAAC 688
OY 127 AAGAGCGTTGAGTGGATTGAGTATTAATCTTAACATGTTGTTACTAATACAGAG 186
DB 687 AAGGAGCTGAGTGGATTGAGTATTTCTTGAGAGGGAGTACTGAATACAAATGAG 628
OY 187 AAGTTCAAGGCAAGGCAATGACTGTAGACAAAGTCTCCAGACAGCTTACATGAG 246
DB 627 AAGTTCAAGGCAAGGCAATGACTGTAGACAAAGTCTCCAGACAGCTTACATGAG 568
OY 247 CTCCGAGCTGACATCTGAGGATTCGAGCTTATTAATCTGCAAGG-----ATAC 299
DB 567 CTCACTAGGCTGACATCTGAGGATTCGAGCTTATTAATCTGCTAGAGGGAGCTACTAT 508
OY 300 TAAGCTCCCTTTGCTTACTAGGCTCCAGAGGACCAAGGTCACCGTCTTCTCAGTGAAG 359
DB 507 AAGGCGTACTTGAATGTTGGGGGCAAGGAGCAACGCTCACGTTCTCTATGTGAGA 448
OY 360 CGGTTCAAGGCGGAGTGGCTCTGGCGGTGGCGGATTCGACATCGAGCTCACTAGTCTCC 419
DB 447 CGGTTCAAGGCGGAGTGGCTCTGGCGGTGGCGGATTCGACATCGAGCTCACTAGTCTCC 388
OY 420 AGCAATCATGTTCTCATCTCCAGGAGGAAAGTCAACATGACCTGCACTGAGCTCAAG 479
DB 387 AGCAATCATGTTCTCATCTCCAGGAGGAGGATCAACATGACCTGCACTGAGCTCAAG 328
OY 480 TATTAAGTTACATGACATCTGTAACAGAGAGCTGTCACTCCCTCCCAAAAGATGATTTA 539
DB 327 TATTAAGTTACATGATTTGTAACAGAGAGCTGTCACTCCCTCCCAAAAGATGATTTA 268
OY 540 TGACATATCCAAATGCGCTTCTGAGAGTCCGTGCTGCTTCACTGAGGAGTGGGTCTGGAC 599
DB 267 TGACATATCCAAATGCGCTTCTGAGAGTCCCTTTTCTGCTTCACTGAGGAGTGGGTCTGGAC 208
OY 600 CTCTTATTTCTCAATCAGACAGCAGTGAAGGCTGTAGATCTGCACTTATTAATCTGCA 659
DB 207 CTCTTATTTCTCAATCAGACAGCAGTGAAGGCTGTAGATCTGCACTTATTAATCTGCA 148
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OY 660 TCAGCGAGTAGTATCCCGCTCACTGCTGCTGAGGACACAGTGGAAATTAACG 717
DB 147 GGAAGTGAAGTGTATTCCTGACACGTTCCGAG-GGGACCAAGCTGAGCTGAACCG 91

RESULT 4

CK629415/c

LOCUS

DEFINITION

AM1-AA0014-041102-021-H09 AA0014 Apis mellifera cDNA, mRNA

sequence.

ACCESSION

CK629415

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

Apis mellifera (honey bee)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea;

Apoidea; Apoidea.

1 (bases 1 to 1419)

NUMES, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,

Matia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,

Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R.,

Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G.,

Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M.,

Espindola, F.S., Peco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and

Silva, M.A. Jr.

Open reading frame ESTs - an efficient strategy for analysis of the

honey bee transcriptome

Unpublished (2004)

CONTACT: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory

Departament of Genetics, FMRP/USP, FUNDHERP

Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639309

Fax: +55 16 39639309

Email: wilsonjr@usp.br

This sequence was derived from the FAPESP Genome Program

High quality sequence start: 63

High quality sequence stop: 605.

Location/Qualifiers

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1..1419
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_id="AA0014"
/note="Organ: whole body"
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ORIGIN

Query Match 57.9%; Score 415; DB 7; Length 1419;
Best Local Similarity 82.9%; Pred. No. 3.2e-111;
Matches 510; Conservative 0; Mismatches 97; Indels 8; Gaps 3;

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OY 108 GGTAAAGCAAGCAGTGAAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 167
DB 703 GGTAAAGCAAGCAGTGAAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 646
OY 168 TGGTACTAATCAATCAAGAGGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 227
DB 645 ANGTACTAATCAATCAAGAGGAGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 586
OY 228 CAGCAGAGCTTACATGAGAGTCCGAGCTGACATCTGAGAGATTCGACATCTTATTAATG 287
DB 585 CAGCAGAGCTTACATGAGAGTCCGAGCTGACATCTGAGAGATTCGACATCTTATTAATG 526
OY 288 TGCAAGG-----ATACATAGGTCCTGTTGCTTACTGAGTCTCAAGGAGGAGGAGGAGGAGG 341
DB 525 TGCTAGAGGAGGAGTCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 466
OY 342 CGTCTCTCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 401
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Db 465 CGTCTCCTCATGTGAGACCGGTTTCAGCGGAGGTGCTGTGCGTGGCCGATCTGCACAT 406
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Db 405 TGAGCTCACCCAGTCTTCACGAAATCATGCTGTGACCTCCAGGAGAGGGGTACACCATGAC 346
QY 462 CTGCAAGTGGAGCTCAAGTATTAATGATCATGCACTGTACACGAGAGAGCTGTCACTTC 521
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QY 522 CCCCCAAAAGATGATTTATATGACACATCCAACTGGCTTCTGAGAGTCCCTGCTGCTTCAG 581
Db 285 CCCCAGCTCTCTATTTATGACATCCAACTGGCTTCTGAGAGTCCCTTTCGCTTCAG 226
QY 582 TGGCAGTGGGTCTGGAGCTCTTATTTCTCACAATGACAGCATGGAGGCTGTAGATGC 641
Db 225 TGGCAGTGGGTCTGGAGCTCTTATTTCTCACAATGACAGCATGGAGGCTGTAGATGC 166
QY 642 TGGCAGTATTTACTGTCATGAGGAGAGTATGTTACCCGCTCAGCTTCGCTGCTGAGCACA 701
Db 165 TGGCAGTATTTACTGTCGACAGAGTGGAGTGTATTCCTATCAGCTTCGAGGAGGAGCACA 106
QY 702 GTTGGAAATATAACG 716
Db 105 GCTGGAGCTGAAACG 91

RESULT 5
CK629414/c 1339 bp mRNA linear EST 26-MAR-2004
LOCUS AM1-AA0014-041102-021-D05 AA0014 Apis mellifera cDNA, mRNA
DEFINITION sequence.

ACCESSION CK629414
VERSION CK629414.1 GI:45753889
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apoidea; Apis.

REFERENCE 1 (bases 1 to 1339)
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Mata,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresifco,E.M.,
Espindola,F.S., Paco-larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.

TITLE Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome

JOURNAL Unpublished (2004)
COMMENT Contact: Silva Jr. W. A.
Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br

FEATURES
source This sequence was derived from the FAPESP Genome Program
High quality sequence start: 62
High quality sequence stop: 662.
Location/Qualifiers
1..1339

/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0014"
/note="Organ: whole body"

ORIGIN

7

Query Match 57.7%; Score 413.6; DB 7; Length 1339;
Best Local Similarity 82.1%; Pred. No. 8,2e-111;
Matches 514; Conservative 0; Mismatches 104; Indels 8; Gaps 3;
QY 100 ATGCACTGGGTGAAGAGAGCCATGGAAGAGCTTTAGTGTGG-AGATATTAATCC 158
Db 715 ATAGCTCGGTGAGCAAGACGCTGAAACAGGACCTTGAGTGGACTGGAATTCGATTTTCC 656
QY 159 TAAATATGATGATCTAATCAATGAGAGAGTTCAAGGGGAGGAGGAGCAATTCGCT-GTGG 217
Db 655 TGGAGAGGGAGATCTGAATATCAATGAGAGAGTTCAAGGGGAGGAGGAGCACTGAGTGTAG 596
QY 218 ACAAGTCTCCAGCAGCAGCTACATGAGAGCTCCGAGCCTGACATCTGAGATTCGAG 277
Db 595 ACAAGTCTCCAGCAGCAGCTAATGAGAGCTCACTGAGAGTCAATCTGAGAGTCTGCTG 536
QY 278 TCTATTACTGTGCAAGAG-----ATATCAAGTCCCGTTTGTCTTACTGGGTCAAGGGA 331
Db 535 TCTATTCTGTGTGATGAGGAGGAGCTAATATAGGCGCTTATCTTGTGCTGAGGAGGGA 476
QY 332 CCAGGCTCACCGCTCTCTAGAGTGGAGGAGGCTTCAGGCGAGGTGCTCTGCGGCTGGCG 391
Db 475 CCAGGCTCACCGCTCTCTATGTGAGGAGGAGGCTTCAGGCGAGGTGCTCTGCGGCTGGCG 416
QY 392 GATCGACATCGAGCTCACTCACTCCAGCATCATCTCTGATCTCCAGGGAGAGAG 451
Db 415 GATCTGACATTTAGAGCTCACCCAGCTCTCCAGCATCATCTCTGATCTCCAGGGAGAGAG 356
QY 452 TCACCATGACCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 511
Db 355 TCACCATGACCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 296
QY 512 CTGTACACCTCCCGCAAAAGATGATTTATGACACATCCAACTGGCTTCTGAGTCCCTG 571
Db 295 CTGTATCTCTCCCGCAACCTCTGATTTATGACACATCCAACTGGCTTCTGAGTCCCTG 236
QY 572 CTGCTTCACTGAGTGGAGTGGAGCTGGAGCTCTTATTTCTGCACTGCACTGCACTGCA 631
Db 235 TTGGCTTCACTGAGTGGAGTGGAGCTGGAGCTCTTATTTCTGCACTGCACTGCACTGCA 176
QY 632 CTGTAGATGCTGCACTTATTTACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 691
Db 175 CTGAGGATGCTGCACTTATTTACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 116
QY 692 CTGGGACACAGTGGAAATATAACG 717
Db 115 GGGGACCAAGCTGAGCTGAAACG 90

RESULT 6
CK633068 672 bp mRNA linear EST 26-MAR-2004
LOCUS AM3-AP0011-151201-021-A08 AP0011 Apis mellifera cDNA, mRNA
DEFINITION sequence.

ACCESSION CK633068
VERSION CK633068.1 GI:45757543
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apoidea; Apis.

REFERENCE 1 (bases 1 to 672)

AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
Mata,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresifco,E.M.,
Espindola,F.S., Paco-larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
Silva,W.A. Jr.
TITLE Open reading frame ESTs - an efficient strategy for analysis of the
honey bee transcriptome
JOURNAL Unpublished (2004)

ORIGIN

COMMENT

Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Department of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Celso Rocco, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonj@usp.br

This sequence was derived from the FAPESP Genome Program
High quality sequence start: 100
High quality sequence stop: 629.

FEATURES

Source

1. 672
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="pupal"
/clone_lib="AP0011"
/note="Organ: whole body"

ORIGIN

Query Match 51.4%; Score 368.2; DB 7; Length 672;
Best Local Similarity 80.7%; Pred. No. 1.9e-97;
Matches 480; Conservative 0; Mismatches 105; Indels 10; Gaps 4;

1 CAGGTGAAGTGCAGCGCTCA-GGACTGAACCTGTGAGCC-TGGGGCTTCAGTGAAGA 58
117 GAGCCATGGAAGAGCCTTGAAGTGTGAGTATTAATCTTAACAATGGTGTACTAA 176
197 GAGCCCTGAACAGGACTTGAAGTGTGAGTATTAATCTTCTGAGAGGGGAGTACTGA 256
177 CTACAGCAAGATTTCAAGGCAAGCCCAATTGACTGTAGACAAGTCTTCCAGACAGC 236
257 ATACAAAGAAAGTTCAAGGCAAGGCGCACACTAGTGTAGACAAGTCTTCCAGACAGC 316
237 CTACATGAGAGTCCGAGCCGATGATGAGATTTGAGATTTGAGTGTAGAG- 295
317 CTATATGAGCTCACTAGGCTGACATCTGAGACTCTGCTGTCTTATTTCTGTGTTAAGG 376
296 -----ATACTACGGTCCCGTTTGCTTACTGGGTCAAGGACACAGGTCACCGTCTCTC 350
377 GGACTACTATAGGGCTACTTTGACTTGTGGGGCCAAAGGACCAAGGTCAACCGTCTCTC 436
351 AGGTGAGGGGTTCAAGCGGAGGTGCTTGGCGGTGGCGGATCGACATCGAGCTCAC 410
437 ATGTGGAGGGGTTCAAGCGGAGGTGCTTGGCGGTGGCGGATCTGACATTTGAGCTCAC 496
411 TCAGTCCAGCAATCATGTCGATCTCCAGGGGAAAGGTCAACATGACCTGCAAGTGG 470
497 CCACTCTCCAGCAATCATGTCGATCTCCAGGGGAAAGGTCAACATGACCTGCAAGTGG 556
471 CAGCTCAAGTAAAGTATACATGACATGACATGACATGACATGACATGACATGACATGAC 530
557 CAGCTCAAGTAAAGTATACATGATTTGGTACCAAGAGCTGGAGTCTTCCCAAGACT 616
531 ATGAGTTTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 585
617 CCGATTTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 671

RESULT 7
CK633069 672 bp mRNA linear EST 26-MAR-2004
LOCUS AM-AP0011-070602-021-A08 AP0011 Apis mellifera cDNA, mRNA
DEFINITION
Sequence.
ACCESSION CK633069

VERSION

CK633069.1 GI:45757544
EST.

KEYWORDS

Apis mellifera (honey bee)

SOURCE

Apis mellifera

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE

Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

AUTHORS

Apidae; Apis.

REFERENCES

1 (bases 1 to 672)

ATTN

Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,

TITLE

Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,

JOURNAL

Monesi, N., Nascimento, A.M., Pelxoto, P.M.V., Silva, M.F.R.,

COMMENT

Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G.,

SOURCE

Zago, M.A., Soares, A.B.E., Bitondi, M.M.G., Espresateco, E.M.,

TITLE

Esposito, F.S., Peco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and

JOURNAL

Silva, W.A. Jr.

COMMENT

Open reading frame ESTs - an efficient strategy for analysis of the

SOURCE

honey bee transcriptome

TITLE

Unpublished (2004)

COMMENT

Contact: Silva Jr, W. A.

SOURCE

Molecular Genetic and Bioinformatics Laboratory

TITLE

Department of Genetics, FMRP/USP, FUNDHERP

COMMENT

Rua Tenente Celso Rocco, 2501, CEP 14051-140, Brazil

SOURCE

Tel: +55 16 39639300

TITLE

Fax: +55 16 39639309

COMMENT

Email: wilsonj@usp.br

SOURCE

This sequence was derived from the FAPESP Genome Program

TITLE

High quality sequence start: 100

COMMENT

High quality sequence stop: 629.

SOURCE

Location/Qualifiers

TITLE

1. 672

COMMENT

/organism="Apis mellifera"

SOURCE

/mol_type="mRNA"

TITLE

/strain="Africanized"

COMMENT

/db_xref="taxon:7460"

SOURCE

/sex="female, worker"

TITLE

/dev_stage="pupal"

COMMENT

/clone_lib="AP0011"

SOURCE

/note="Organ: whole body"

ORIGIN

Query Match 51.4%; Score 368.2; DB 7; Length 672;
Best Local Similarity 80.7%; Pred. No. 1.9e-97;
Matches 480; Conservative 0; Mismatches 105; Indels 10; Gaps 4;

1 CAGGTGAAGTGCAGCGCTCA-GGACTGAACCTGTGAGCC-TGGGGCTTCAGTGAAGA 58
117 GAGCCATGGAAGAGCCTTGAAGTGTGAGTATTAATCTTAACAATGGTGTACTAA 176
197 GAGCCCTGAACAGGACTTGAAGTGTGAGTATTAATCTTCTGAGAGGGGAGTACTGA 256
177 CTACAGCAAGATTTCAAGGCAAGCCCAATTGACTGTAGACAAGTCTTCCAGACAGC 236
257 ATACAAAGAAAGTTCAAGGCAAGGCGCACACTAGTGTAGACAAGTCTTCCAGACAGC 316
237 CTACATGAGAGTCCGAGCCGATGATGAGATTTGAGATTTGAGTGTAGAG- 295
317 CTATATGAGCTCACTAGGCTGACATCTGAGACTCTGCTGTCTTATTTCTGTGTTAAGG 376
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377 GGACTACTATAGGGCTACTTTGACTTGTGGGGCCAAAGGACCAAGGTCAACCGTCTCTC 436
351 AGGTGAGGGGTTCAAGCGGAGGTGCTTGGCGGTGGCGGATCGACATCGAGCTCAC 410
437 ATGTGGAGGGGTTCAAGCGGAGGTGCTTGGCGGTGGCGGATCTGACATTTGAGCTCAC 496
411 TCAGTCCAGCAATCATGTCGATCTCCAGGGGAAAGGTCAACATGACCTGCAAGTGG 470

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QY      471  CAGCTCAAGATATAGTTACATGACCTGATCCAGCAAGACCTGTCACTCCCCCAAAAG 530
Db      557  CAGCTCAAGATATAGTTACATGATATATGATCAACAGAAAGCCGTGATCTCCCCCAACT 616
QY      531  ATGATTTATATGACATCCAACTGGCTTCTGAGATCCCTGCTGCTTCACTGAGTGC 585
Db      617  CCTGATTATATGACATCCAACTGGCTCTGAGATCCCATTTTCGCTTCACTGAGTGC 671

RESULT 8
CK629843      963 bp      mRNA      linear      EST 26-MAR-2004
LOCUS      CK629843/c
DEFINITION  AM2-AA0023-091202-021-H05 AA0023 Apis mellifera cDNA, mRNA
sequence.
ACCESSION  CK629843
VERSION    CK629843.1  GI:45754318
KEYWORDS   EST.
SOURCE     Apis mellifera (honey bee)
ORGANISM   Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1 (bases 1 to 963)
            Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
            Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
            Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
            Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
            Zago,M.A., Soares,A.E.B., Bitondi,M.M.G., Espreefco,E.M.,
            Espindola,F.S., Paco-larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
            Silva,W.A. Jr.
            Open reading frame ESTs - an efficient strategy for analysis of the
            honey bee transcriptome
            Unpublished (2004)
            Contact: Silva Jr, W. A.
            Molecular Genetic and Bioinformatics Laboratory
            Department of Genetics, FMRP/USP, FUNDHERP
            Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
            Tel: +55 16 39639300
            Fax: +55 16 39639309
            Email: wilsonjr@usp.br
            This sequence was derived from the FAPESP Genome Program
            High quality sequence start: 88
            High quality sequence stop: 376.
FEATURES
            source
            1..963
            /organism="Apis mellifera"
            /mol_type="mRNA"
            /strain="Africanized"
            /db_xref="taxon:7460"
            /sex="female, worker"
            /dev_stage="adult"
            /clone_lib="AA0023"
            /note="Organ: whole body"

ORIGIN
Query Match      48.1%; Score 344.6; DB 7; Length 963;
Best Local Similarity 82.0%; Pred. No. 2e-90;
Matches 460; Conservative 0; Mismatches 89; Indels 12; Gaps 5;

QY      166  GGTGACTAATCAACAGAGGTTCAAGGGCAAGGCCACATTTGACTGTAGCAAGTCC 225
Db      644  GGGGATGCTGAGTACATGAGAA-TTCAATGGCAAGGCCCACTGAGTGTAGCAAGTCC 586
QY      226  TCCAGACACAGCCCTACATGAGCTCCGACGCTGACATCTGAGGATTCGACGCTTA-TTA 284
Db      585  TCCAGACACAGCCCTATATGAGCTCACAAGGCTGACATCTGAGGACCTCTGCTGCTATTG 526
QY      285  CTGTGCAAGAG-----ATACTACGATCCCGTTTGGTTTACTGCTGCTCAAGGACCA-G 336
Db      525  CTGTGCTAGAGGGGAGGAGTACTATAGGCGCTACTTTGACTTGTGCGGCTCAAGGACCAAG 466
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QY      337  GTCAACGTTCTCTCAGATGAGAGGCGGTTTCAGGCGAGTGGCTTGGCGGTGCGGATCG 396
Db      465  GTCAACGTTCTCTCAGATGAGAGTCCGTTTCAGGCGAGAGTGGCTTGGCGGTGCGGATCT 406
QY      397  GACATGAGCTCACTCAGTCTCCAGCAATCATGCTGATCTTCCAGAGGAGAGAGTCAACC 456
Db      405  GACATGAGCTCAACCAAGTCTCCAGCAATCATGCTGATCTTCCAGAGGAGAGAGTCAACC 346
QY      457  ATGACCTGAGTGGAGAGCTCAAGTATATAGTTATCATGCACTGGTATACAGAGAACCTGTC 516
Db      345  ATGACCTGAGTGGAGAGCTCAAGTATATAGTTATCATGCACTGGTATACAGAGAACCTGTA 286
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Db      285  TCTCTCCCCAGACTCCTATATGATACATCCAACTGGCTTGGAGTCCCTTTTCCG 226
QY      577  TTCACTGGAGTGGGTGGGACCTTTATTTCTTTCACAAATGACAGCATGAGAGCTGTA 636
Db      225  TTCAGTGGAGTGGGTGGGACCTTTATTTCTTTCACAAATGACAGAGGAGCTGAG 166
QY      637  GATGCTGCCACTTATTTATCTGCATCAGCGAGATAGTTACCGCTACCGTTCGTGGG 696
Db      165  GATGCTGCCACTTATTTATCTGCAGAGAGTGGAGTGTATCCGTACACTTCGAGAG--GGG 108
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Db      107  ACCAAGCTGGAAGTGAACGG 87

RESULT 9
CK632348      823 bp      mRNA      linear      EST 26-MAR-2004
LOCUS      CK632348
DEFINITION  AM0-AM0009-070103-021-H02 AM0009 Apis mellifera cDNA, mRNA
sequence.
ACCESSION  CK632348
VERSION    CK632348.1  GI:45756823
KEYWORDS   EST.
SOURCE     Apis mellifera (honey bee)
ORGANISM   Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1 (bases 1 to 823)
            Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
            Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
            Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
            Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
            Zago,M.A., Soares,A.E.B., Bitondi,M.M.G., Espreefco,E.M.,
            Espindola,F.S., Paco-larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
            Silva,W.A. Jr.
            Open reading frame ESTs - an efficient strategy for analysis of the
            honey bee transcriptome
            Unpublished (2004)
            Contact: Silva Jr, W. A.
            Molecular Genetic and Bioinformatics Laboratory
            Department of Genetics, FMRP/USP, FUNDHERP
            Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil
            Tel: +55 16 39639300
            Fax: +55 16 39639309
            Email: wilsonjr@usp.br
            This sequence was derived from the FAPESP Genome Program
            High quality sequence start: 70
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FEATURES
            source
            1..823
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            /mol_type="mRNA"
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            /db_xref="taxon:7460"
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            /dev_stage="Mix of adult, pupal, larval and embryonic."
            /clone_lib="AM0009"
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ORIGIN

/note="Organ: whole body"

Query Match 48.0%; Score 344; DB 7; Length 823;
 Best Local Similarity 78.5%; Pred. No. 2.9e-90;
 Matches 489; Conservative 0; Mismatches 118; Indels 16; Gaps 6;

1 CAGGTGAAGCTGAGCAGTCAAGACCTGAACTGGTGAAGCTGGGGCTTCAAGTAATA 60
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 61 TCTGCAAGACTTCTGGGAAACAATTCATGAATACACATGACATGAGTGAAGCAGC 120
 162 TCTGCAAGACTTCTGGGAAACAATTCATGAATACACATGAGTGAAGCAGCAGC 221
 121 CAGTGAAGACCTTGAAGTGAATGATTAATCTTAACAATGGTGTACTTAATAC 180
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 181 AAGCAGAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 282 AAGCAGAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 341
 241 AAGCAGAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 295
 342 AAGCAGAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 401
 296 -ATACTAAGCTCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 354
 402 TACTATAGGCGCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 461
 355 GAGAGCGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 414
 462 GAGAGCGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 521
 415 TCTCAGACAACTCAATGCTGATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 472
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 533 GGTCAAGTATATAGTCAATGCTGATCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 592
 642 TGA-TTATGACACATC--AAGTGGCCCTGAGTCTTTCGCT--TGAAGGAGGAGG-- 693
 593 CTGGAGCTCTTATTTCTCTGACA 615
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 LOCUS BQ328142
 DEFINITION M4-R0048-210201-003-e06 R0048 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BQ328142
 VERSION BQ328142.1 GI:20946291
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
 1 (bases 1 to 567)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H.,
 Brunser, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the PABSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-R0048-
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 Seq primer: puc 18 forward.

FEATURES

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 /organism="Homo sapiens"
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 /note="Organ: Kidney tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 46.9%; Score 336.4; DB 5; Length 567;
 Best Local Similarity 81.5%; Pred. No. 4.6e-88;
 Matches 440; Conservative 0; Mismatches 91; Indels 9; Gaps 4;

167 GTGTAATTAATCAAGCAGAACTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 226
 562 GAGGAGTAATCAATGATGAGACTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503
 227 CAGCAGAGCTTCAATGAGAGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 286
 502 GAGCAGAGCTTCAATGAGAGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443
 287 GTGCAAGAG-----ATACTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 340
 442 GTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383
 341 CCGTCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
 382 CCGTCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459
 400 ATGAGGCTCACTAGTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459
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 142 AGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 83
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 82 GGTGCACTTATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 25

RESULT 11

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 LOCUS BI030095 585 bp mRNA linear EST 14-JUN-2001
 DEFINITION IL0-MT0355-220301-500-d11 MT0355 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI030095
 VERSION BI030095.1 GI:14436725
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 585)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&ct=IL0-MT0355-220301-500-d1&ct3=2001-03-22&ct4=1)
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 /note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORFESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ORIGIN
 Query Match 45.9%; Score 329.4; DB 4; Length 585;
 Best Local Similarity 82.2%; Pred. No. 5.5e-86;
 Matches 405; Conservative 0; Mismatches 81; Indels 7; Gaps 2;
 QY 231 CACAGCCTACATGAGTCCGACGCCGACATCTGAGAGATTCTGCACTTATTAAGTGC 230
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 DB 465 CTCCTATATGAGAGCGGTTCAAGCGGAGGTGCTGAGCGGTGGCGGATCTGACATGGA 406
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 DB 285 CAGACTCCGATTTATGACACATCCAACTGGCTTCTGAGATCCCTGCTGCTTCAATG 226
 QY 585 CAGTGGGTGGGAGCCTTTATTTCTCACAATCAGACAGATGAGAGGCTGTAGATGTCG 644
 DB 225 CAGTGGGTGGGAGCCTTTATTTCTCACAATCAGACAGATGAGAGGCTGTAGATGTCG 166
 QY 645 CACTTATTAATCTCCATCAGCGGAGTATCCCGCTCAGTTCGCTGGAGACACAGTT 704
 DB 165 CACTTATTAATCTCCAGAGATGAGTGTATCCGTACAGATTCGAG- GGGAGACCAAGCT 107
 QY 705 GGAATTAACCG 717
 DB 106 GGAGCTGAACCG 94
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 DEFINITION QV4-NT0248-271100-585-c10 NT0248 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF923394
 VERSION BF923394.1 GI:12319282
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 476)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&ct=QV4-NT0248-271100-585-c10&ct3=2000-11-27&ct4=1)
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 FEATURES
 source

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 43.7%; Score 313; DB 2; Length 488;
Best Local Similarity 87.3%; Pred. No. 3.7e-81;
Matches 343; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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QY 385 GGTGGGAGTCCGACATTCAGCTCAGTCTCCAGCAATCATGTCGTGATCCAGG 444
DB 428 GATGGGAGTCCGACATTCAGCTCAGTCTCCAGCAATCATGTCGTGATCCAGG 369
QY 445 GAGAAAGTCAACATGACCTGACAGTGGCAGCTCAAGTAAAGTACATGCACTGTAACAG 504
DB 368 GAGAGGCTCAACATGACCTGACAGTGGCAGCTCAAGTAAAGTACATGTAACAG 309
QY 505 CAGAAAGTCAACCT 564
DB 308 CAGAAAGTCAACCT 249
QY 565 GTCCCTGCTGCTTCAAGTGGCAGTGGGTCCTTATTTCTCTCAATCAGACAGC 624
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QY 625 ATGAGGCTGTATAGTCTGCACTTATTAATGACATGAGGAGTGAACCCGCTCAG 684
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QY 685 TTCGCTGTGGGACACAGTTGAATPAAACGG 717
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ACCESSION B0373705
VERSION B0373705.1 GI:21049219
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 427)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Dias Neto E., Garcia Correa, R., Varjovski-Almeida, S., Briones, M.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV1&t2=QV1-PT0170-
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High quality sequence stop: 426.
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/db_xref="taxon:9606"
/dev_stage="Adult"
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/note="Organ: prostate tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 42.9%; Score 307.8; DB 5; Length 427;
Best Local Similarity 85.9%; Pred. No. 1.2e-79;
Matches 367; Conservative 0; Mismatches 52; Indels 8; Gaps 2;
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QY 334 AAGGCT--CAGGCTCTCAGGTGAGGAGGCTTCAAGGAGGAGGAGGCTGCGGAGGCG 391
DB 307 AAGGCTCAACCGCTCTCTATGAGGAGGCTTCAAGGAGGAGGAGGCTGCGGAGGCG 248
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DB 247 GATCTGACATGAGCTCACTCACTGCTCCAGCAATGATCTGATCTCCAGGAGGAGAG 188
QY 452 TCACCATGACCTGACAGTGGCAGCTCAAGTATAGTTACATGCACTGCTGACAGCAGAAC 511
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QY 512 CTGTACACCTCCCAAAAGATGATTTATGACATCCAACTGGCTTGGAGTCCCTG 571
DB 127 CTGTATCTCTCCCAAGACTCTGATTTATGACATCCAACTGGCTTGGAGTCCCTG 68
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Db 67 TTGCTTCAGTGGCAGTGGTCTGGACCTCTTATTCTCTCACAATCAACCGAATGGAG 8

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Db 7 CTGAGA 1

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 18:39:34 : Search time 3216.24 Seconds
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Title: US-10-075-947A-2

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg: *
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12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	714	100.0	1173	6 AR231457	AR231457 Sequence
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5	478	66.9	1389	6 BD222936	BD222936 Heteromn
6	478	66.9	1389	6 AX023361	AX023361 Sequence
7	475.2	66.5	1380	6 CO856167	CO856167 Sequence
8	432	60.5	738	10 MUSVRLI	L41689 Mus musculu
9	417.2	58.4	840	10 MM295476	Z55476 Mus musculu
10	414.4	58.0	752	6 AR481833	AR481833 Sequence
11	414.4	58.0	1509	6 AR481832	AR481832 Sequence
12	414.4	58.0	1527	6 AR481831	AR481831 Sequence
13	408.2	57.2	729	6 AR364987	AR364987 Sequence
14	407.8	57.1	1632	12 SYN507107	AS507107 Synthetic
15	400.2	56.1	824	6 AR481837	AR481837 Sequence
16	399	55.9	743	12 SYN7A41	M68968 Synthetic
17	398.2	55.8	737	6 A62066	A62066 Sequence 1
18	398.2	55.8	737	6 A66041	A66041 Sequence 23
19	398.2	55.8	737	6 AR088010	AR088010 Sequence

20	398.2	55.8	737	6 AR154831	AR154831 Sequence
21	396.2	55.5	738	6 E07990	E07990 DNA encodin
22	396.2	55.5	738	6 I45910	I45910 Sequence 6
23	394.8	55.3	734	6 AR343614	AR343614 Sequence
24	393.6	55.1	720	6 AR364986	AR364986 Sequence
25	393.2	55.1	739	6 A95266	A95266 Sequence 12
26	393.2	55.1	739	6 BD226888	BD226888 Improve
27	393.2	55.1	739	6 AR306901	AR306901 Sequence
28	389.2	53.7	1931	6 AX590282	AX590282 Sequence
29	352.6	49.4	855	10 MUSALCA	L43544 Mus musculu
30	351	49.2	824	12 SYNMA15C5	M69286 Recombinant
31	351	49.2	1701	12 SYNCH1PL	M69273 Cloning vec
32	347	48.6	1701	12 SC0564232	AX564232 Synthetic
33	336.6	47.1	796	6 BD222932	BD222932 Heteromn
34	336.6	47.1	796	6 AX023355	AX023355 Sequence
35	323.6	45.3	354	10 MUSIGHMT	M36228 Mouse Ig he
36	318	44.5	420	6 AR169919	AR169919 Sequence
37	318	44.5	420	6 AR365720	AR365720 Sequence
38	317.2	44.4	371	12 AY648618	AY648618 Mus muscu
39	317.2	44.4	372	12 AY648617	AY648617 Mus muscu
40	314.8	44.1	345	10 MUSIGMO520	M76414 Mouse IgM c
41	313.4	43.9	444	12 AY648611	AY648611 Mus muscu
42	312.8	43.8	1056	6 AX363232	AX363232 Sequence
43	312.8	43.8	1411	6 AX363234	AX363234 Sequence
44	312.8	43.8	1702	6 AX363235	AX363235 Sequence
45	310.8	43.5	360	10 MUSIGHADX	M36217 Mouse Ig he

ALIGNMENTS

RESULT 1
AR231455
LOCUS AR231455 Sequence 2 from patent US 6451995.
DEFINITION AR231455
ACCESSION AR231455
VERSION AR231455.1 GI:27272557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 714)
AUTHORS Cheung,N.-K.V., Larson,S.M., Guo,H.-F., Rivlin,K. and Sadelain,M.
TITLE Single chain Fv polynucleotide or peptide constructs of anti-ganglioside GD2 antibodies, cells expressing same and related methods
JOURNAL Patent: US 6451995-A 2 17-SEP-2002;
FEATURES
ORIGIN Location/Qualifiers
source 1..714
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 714; DB 6; Length 714;
Best Local Similarity 100.0%; Pred. No. 9.1e-179;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGTATTGATGATGACCCAGACTCCCAANTTCCTGCTTGATAGACAGAGAGGTTACC 60
DB 1 AGTATTGATGATGACCCAGACTCCCAANTTCCTGCTTGATAGACAGAGAGGTTACC 60
OY 61 ATAACTGCAAGGCGACGATGAGTGAATATGATGCTTGATCCACACAGAGCA 120
DB 61 ATAACTGCAAGGCGACGATGAGTGAATATGATGCTTGATCCACACAGAGCA 120
OY 121 GGGCAGTCCCGAAGTGTGATATCTGATCATCAATCGCTACACTGAGTCCCTGAT 180
DB 121 GGGCAGTCCCGAAGTGTGATATCTGATCATCAATCGCTACACTGAGTCCCTGAT 180
OY 181 CGCTTCACTGCGACGTGATATGAGACGATTTCACTTTACCATCAGACACTGTGAGGCT 240
DB 181 CGCTTCACTGCGACGTGATATGAGACGATTTCACTTTACCATCAGACACTGTGAGGCT 240

QY	241	GAAGACCTGGAGATTATTTCTGTCAGAGAGATTATGCTGCTCGAGGGGGGACCAAG	300
Db	241	GAAGACCTGGCACTTTATTTCTGTGACAGAGATTATTAAGCTGCTCGAGGGGGGACCAAG	300
QY	301	CTGGAAATTAAGGTGAGCGGTTCTAGCCGAGAGTGGCTCTGGCGGTGAGCATCGCAG	360
Db	301	CTGGAAATTAAGGTGAGCGGTTCTAGCGCGGATCGAGGTGGCTCTGGCGGTGAGCATCGCAG	360
QY	361	GTCGAGGTGAAGAGTCAGGACCTGGCTGGTGGCGCCCTCAAGAGCTTGTCCATCACT	420
Db	361	GTCGAGGTGAAGAGTCAGGACCTGGCTGGTGGCGCCCTCAAGAGCTTGTCCATCACT	420
QY	421	TGCATGCTCTCGGGTTTTCAATTAAACCAATTATGTTGACACTGGGGTTGCGCAGCCTCA	480
Db	421	TGCATGCTCTCGGGTTTTCAATTAAACCAATTATGTTGACACTGGGGTTGCGCAGCCTCA	480
QY	481	GGAAGGGTCTGAGTGGCTGGAGTAATATGGCGTGGTGAAGCACAAATTAATTAATTCG	540
Db	481	GGAAGGGTCTGAGTGGCTGGAGTAATATGGCGTGGTGAAGCACAAATTAATTAATTCG	540
QY	541	GCTCTTAATGTCACACTGAGCATCAGCAAGGACAACTCCAGAGCGCAAGTTTCTTAATAA	600
Db	541	GCTCTTAATGTCACACTGAGCATCAGCAAGGACAACTCCAGAGCGCAAGTTTCTTAATAA	600
QY	601	ATGAACAGTCTGCAACTGATGACACAGCCATGTACTATCTGTGCACAGTCGGGGGGGTAAAC	660
Db	601	ATGAACAGTCTGCAACTGATGACACAGCCATGTACTATCTGTGCACAGTCGGGGGGGTAAAC	660
QY	661	TACGGCTATGCTTTGGACTACTAGGGGTCAAGAACTCAAGCACCGTCTCTCTCA	714
Db	661	TACGGCTATGCTTTGGACTACTAGGGGTCAAGAACTCAAGCACCGTCTCTCTCA	714

RESULT 2			
AR231457			
LOCUS	AR231457	1173 bp	DNA
DEFINITION	Sequence 4 from patent US 6451995.	linear	PAT 20-DEC-2002
ACCESSION	AR231457		
VERSION	AR231457.1	GI:27272559	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1173)		
TITLE	Cheung,N.-K.V., Larson,S.M., Guo,H.-F., Rivlin,K. and Sadelain,M. Single chain Fv polynucleotide or peptide constructs of anti-ganglioside Gm2 antibodies, cells expressing same and related methods		
JOURNAL	Patent: US 6451995-A 4 17-SEP-2002;		
FEATURES	Location/Qualifiers		
SOURCE	1..1173		
	/organism="unknown"		
	/mol_type="genomic DNA"		

Query Match	100.0%	Score 714;	DB 6;	Length 1173;
Best Local Similarity	100.0%	Pred. No. 8,8e-179;		
Matches 714;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	AGATTGTGATGACCCAGACTCCCAAAATTCGTGCTGTATATAGACAGAGACAGGGTTAAC	60
Db	1	AGATTGTGATGACCCAGACTCCCAAAATTCGTGCTGTATATAGACAGAGAGACGGGTTAAC	60
Qy	61	ATTAACCTGCAGAGGCCAAGTCAGAGTGTGAGTATGATGTGTGGTATCCAAACAGAGCCA	120
Db	61	ATTAACCTGCAGAGGCCAAGTCAGAGTGTGATATATGTGTGGTATCCAAACAGAGCCA	120
Qy	121	GGGCAAGTCTCCGAAGACTGATATATCTCTGCATCCATCGCTACACTGGAGTCCCTGAT	180
Db	121	GGGCAAGTCTCCGAAGACTGATATATCTCTGCATCCAAATCGCTACACTGGAGTCCCTGAT	180
Qy	181	CGCTTCACTGCGACGTGATATGGACGAGTTTCACTTCAACCATCAGCACTGTGCAGGCT	240

Db	18	CGCTTCACTGCGACAGTGATATGGAGACGAAATTTCACCTTCCACATCAGCACTGTGCAGGCT	240
Qy	241	GAAGACCTGGCAGTTTATTTCTGTCAACAGAGATTTATAGCTCGCTCGAGAGGGGGGACCAAG	300
Db	241	GAAGACCTGGCAGTTTATTTCTGTCAACAGAGATTTATAGCTCGCTCGAGAGGGGGGACCAAG	300
Qy	301	CTGGAATTAATAAGGTGAGCGGTTCCAGCGGAGAGTGGCTCTGGCGGTGCGGATCGCAG	360
Db	301	CTGGAATTAATAAGGTGAGCGGTTCCAGCGGAGAGTGGCTCTGGCGGTGCGGATCGCAG	360
Qy	361	GTGCAAGTGAAGAGTCAAGACCTGGCTGTGGCGCCCTTCACAGAGCTGTTCATCACT	420
Db	361	GTGCAAGTGAAGAGTCAAGACCTGGCTGTGGCGCCCTTCACAGAGCTGTTCATCACT	420
Qy	421	TGCACTGTCTCTGGGTTTTCAATTAACCAATTATGGTGTACACTGGGTTTGGCCAGCCCTCA	480
Db	421	TGCACTGTCTCTGGGTTTTCAATTAACCAATTATGGTGTGTACACTGGGTTTGGCCAGCCCTCA	480
Qy	481	GGAAGGGGTCTGAGTGGCTGAGAGTAATAATGGGCTGTGGAGAACCAAAATTATTAATTCG	540
Db	481	GGAAGGGGTCTGAGTGGCTGAGAGTAATAATGGGCTGTGGAGAACCAAAATTATTAATTCG	540
Qy	541	GCTTTTATGTCCAGACTGAGCACTACAGAAAGACAACCTCCAGAGCCAAAGTTTCTTTAAAA	600
Db	541	GCTTTTATGTCCAGACTGAGCACTACAGAAAGACAACCTCCAGAGCCAAAGTTTCTTTAAAA	600
Qy	601	ATGAACAGTCTGCAAACTGATGACACAGACCATGTACTACTGTGCACAGTCGGGGGGGTAAAC	660
Db	601	ATGAACAGTCTGCAAACTGATGACACAGACCATGTACTACTGTGCACAGTCGGGGGGGGTAAAC	660
Qy	661	TACGGCTATGTCTTTGGACTACTGAGGGGTCAAGAAACCTCACTCACTGCTCTCTCA	714
Db	661	TACGGCTATGTCTTTGGACTACTGAGGGGTCAAGAAACCTCACTCACTGCTCTCTCA	714

RESULT 3				
BD222935				
LOCUS	BD222935	1371 bp	DNA	linear
DEFINITION	Heteromimbodites.			
ACCESSION	BD222935			
VERSION	BD222935.1	GI:33032705		
KEYWORDS	JP 2002521053-A/29.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1371)			
AUTHORS	Kiefer, P., Dreier, T., Baeuerle, P. A., Borschert, K. and Zettl, F.			
TITLE	Heteromimbodites			
JOURNAL	Patent: JP 2002521053-A 29 16-JUL-2002;			
COMMENT	MICROMET AG			
	OS Homo sapiens (human)			

PF 28-JUL-1999 JP 2000562401
PR 28-JUL-1998 EP 98114082.5
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN
BORSCHERT.

	FEATURES	SOURCE
FT	Key	Location/Qualifiers (10) . . (1359) .
CDS	Location/Qualifiers	1. .1371
	/organism="Homo sapiens"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	

ORIGIN

Query Match 66.9%; Score 478; DB 6; Length 1371;
Best Local Similarity 81.5%; Pred. No. 4.8e-116;
Matches 585; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

3 TATGTGATGATGACCCAGACTCCCAATTCCTGCTGTATGACAGAGAGACAGAGTTACCAT 62
Db TATCAGCTGACCCAGCTCTCAAAATTCATTCATCCATCAGTAGAGACAGAGTCCAGCT 128
63 AACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 122
Db CACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 188
129 CACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 188
123 GCACTGCTCCGAATCTGTATATCTGTGATGATGATGATGATGATGATGATGATGATGAT 182
189 GCAATCTCTTAACACATGATTTACTGCGGCTTACCGGATGATGATGATGATGATGATGAT 248
183 CTTTACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 242
249 CTTTACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 308
243 AGACCTGCAAGTATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 293
309 AGACTTGGCAGAGATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
294 GACCAAGCTGGAATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 353
369 GACCAAGCTGGAATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
354 ATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
429 TTTTACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
414 CATCACTGCAAGTATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 473
489 CATCACTGCAAGTATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
474 GCTTCCAGGAAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
549 GTCTCCAGGAAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608
534 TAAATGCGCTTTATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593
609 TAAATGCGCTTTATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
594 CTTAAATGATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653
669 CTTTAAATGATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
654 GGGTAACTACGGCTATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
728 -----AGAACTGCTGCTTGTGCTTACTGCGGCAAGGACCAACGCTGACCGTCTCC 777

RESULT 4
AX023359 1371 bp DNA linear PAT 15-SEP-2000
LOCUS Sequence 30 from Patent MO0006605.
DEFINITION AX023359
ACCESSION AX023359
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kufner P., Zettl F., Dreier T., Bauearle P.A. and Borschert K.
Heteromimibodies
Patent: WO 0006605-A 30 10-FEB-2000;
KUFER PETER (DE); ZETTL FLORIAN (DE); DREIER TORSTEN (DE);
BAUEARLE PATRICK A (DE); BORSCHERT KATHRIN (DE); MICROMET GES FUER
BIOMEDIZINIS (DE)

FEATURES
Source

1. 1371
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
10. 1362
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/protein_id="CAC08832.1"
/db_xref="GI:10183772"
/translation="MGMSCLILPLVATNGVHSDILOLOSQKEMSTSVGRVSTCKA
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ITCTVGSFSLTSYGVHVRQSPKGLFEMLVISVSGSDYDVAAPFISRLSISKNSXS
VFPRMSLQANDRALITYCARMEMSPRYMGOQTVTVSEPRKSTPFGSGSEBELK
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NGNNVKNPLTLMPLTFKPMKPAKTELKLEILKGGSGGSGGSGGVKLOESPGVQVPSQSL
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ORIGIN

Query Match 66.9%; Score 478; DB 6; Length 1371;
Best Local Similarity 81.5%; Pred. No. 4.8e-116;
Matches 585; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

3 TATGTGATGATGACCCAGACTCCCAATTCCTGCTGTATGACAGAGAGACAGAGTTACCAT 62
Db TATCAGCTGACCCAGCTCTCAAAATTCATTCATCCATCAGTAGAGACAGAGTCCAGCT 128
63 AACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 122
Db CACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
129 CACCTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
123 GCACTGCTCCGAATCTGTATATCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 182
189 GCAATCTCTTAACACATGATTTACTGCGGCTTACCGGATGATGATGATGATGATGATGATGAT 248
183 CTTTACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 242
429 TTTTACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
414 CATCACTGCAAGTATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 473
489 CATCACTGCAAGTATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
474 GCTTCCAGGAAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
549 GTCTCCAGGAAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608
534 TAAATGCGCTTTATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593
609 TAAATGCGCTTTATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
594 CTTAAATGATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653
669 CTTTAAATGATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
654 GGGTAACTACGGCTATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
728 -----AGAACTGCTGCTTGTGCTTACTGCGGCAAGGACCAACGCTGACCGTCTCC 777

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RESULT 5
BD222936
LOCUS      BD222936                1389 bp    DNA          linear    PAT 17-JUL-2003
DEFINITION Heteromimibodies.
ACCESSION  BD222936
VERSION    BD222936.1  GI:33032706
KEYWORDS   JP 2002521053-A/30.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 1389)
AUTHORS    Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
TITLE      Heteromimibodies
JOURNAL    Patent: JP 2002521053-A 30 16-JUL-2002;
            MICROMET AG
COMMENT    OS Homo sapiens (human)
            PN JP 2002521053-A/30
            PD 16-JUL-2002
            PE 28-JUL-1999 JP 2000562401
            PR 28-JUL-1998 EP 98114082.5
            PI PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI FLORIAN ZETTL
            PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC C07K19/00.
            PC C12N5/10,C12P21/02,G01N33/53,G01N33/53// (C12N5/10,C12R1:91),
            PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC (C12N5/00,C12R1:91)
            CC Heteromimibodies
            FH Key
            FT CDS Location/Qualifiers
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ORIGIN
Query Match      66.9%; Score 478; DB 6; Length 1389;
Best Local Similarity 81.5%; Pred. No. 4.8e-116;
Matches 585; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY      3 TATTGTGATGACCCAGACTCCCAATTCCTGCTGTATGACGAGGAGACGAGGTTACCAT 62
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DB      69 TATTCACCTAACCCAGTCTCAAAAATTCATGTCACATCGTAGAGACAGGGTCAAGCT 128
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      63 AACCTGCAAGCCAGTCAGAGTGTAGTAATGATGTGGCTTGATCCACAGACAGCCAG 122
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      129 CACCTGCAAGCCAGTCAGAGTGTAGTAATGATGTGGCTTGATCCACAGACAGCCAG 188
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      123 GCAGTCTCCGAATCTGTATATCTCTGCATCCATCGCTCACTGAGAGTCCCTGATCG 182
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      189 GCATCTCCCTAAAGCACTGATTTACTCGGCATCTTACCGGTAAAGTAGAGTCCCTGATCG 248
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      183 CTTCACTGAGGAGTATATGAGGACGATTCACTTTCACATGACATGACATGTCGACGCTGA 242
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      249 CTTCACTGAGGAGTATATGAGGACGATTCACTTTCACATGACATGACATGTCGACGCTGA 308
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      243 AGAAGCTGAGGAGTATATCTGTGACGAGATTAAGCT-----CGCTCGAGAGGGG 293
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      309 AGAAGCTGAGGAGTATATCTGTGACGAGATTAAGCT-----CGCTCGAGAGGGG 368
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      294 GACCAAGCTGGAATTAAGAGTGAAGCGGCTTCAAGCGAGAGTGGCTCTGCGAGTGGCGG 353
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      369 GACCAAGCTGGAATTAAGAGTGAAGCGGCTTCAAGCGAGAGTGGCTCTGCGAGTGGCGG 428
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      354 ATGCGAGGTGACAGTGAAGAGTCAAGACCTTGCGCTGTGTGGCCCTCACAAGAGCCGTGC 413
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      429 TTCTCAGGTGAATCTGAGAGTCAAGACCTTGCGCTGTGTGTGACAGCCCTCACAAGAGCCGTGC 488
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QY      414 CATCACTTGACATGCTCTGAGGTTTTCATTAACCAATTAATGTGTACACTGGGTTGCCA 473
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DB      489 CATCACTTGACATGCTCTGAGGTTTTCATTAACCAATTAATGTGTACACTGGGTTGCCA 548
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      474 GCTTCCAGGAAGAGGTTCTGAGTGGCTGGAGATTAATGTGGCTGTGTGGAAGCACAATTA 533
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      549 GTCTCCAGGAAGAGGTTCTGAGTGGCTGGAGATTAATGTGGCTGTGTGGAAGCACAATTA 608
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      534 TAAATGCGCTCTATGTCCAGATGACATGACATGACAGCAAGCAACTCCAGAGCCAGTTT 593
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      609 TAAATGAGCTTTATATTCAGATGACATGACATGACAGCAAGCAACTCCAGAGCCAGTTT 668
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      594 CTTAAATTAAGACAGTCTGCAATCTGATGACACAGCCATGTACTAGTGGCAGTGGGG 653
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      669 CTTAAATTAAGACAGTCTGCAATCTGATGACACAGCCATGTACTAGTGGCAGTGGGG 727
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      654 GGGTAAGTACGGGTATGCTTTGGACATCTAGTGGGGTCAAGAACTCAGTCAAGCTCTCC 711
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      728 -----AGAACTGGTGGTTGCTTACCTGGGGCCAAAGGACCAACGATCAGCTCTCC 777
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
AX023361
LOCUS      AX023361                1389 bp    DNA          linear    PAT 15-SEP-2000
DEFINITION Sequence 32 from Patent WO0006605.
ACCESSION  AX023361
VERSION    AX023361.1  GI:10183773
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1
AUTHORS    Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
TITLE      Heteromimibodies
JOURNAL    Patent: WO 0006605-A 32 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GRS FUER
            BIOMEDIZINIS (DE)
FEATURES
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ORIGIN
Query Match      66.9%; Score 478; DB 6; Length 1389;
Best Local Similarity 81.5%; Pred. No. 4.8e-116;
Matches 585; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY      3 TATTGTGATGACCCAGACTCCCAATTCCTGCTGTATGACGAGACAGAGGTTTACCAT 62
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DB      69 TATTCACCTAACCCAGTCTCAAAAATTCATGTCACATGAGTAGAGACAGGGTCAAGCT 128
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QY      63 AACCTGCAAGCCAGTCAGAGTGTAGTAATGATGTGGCTTGATCCACAGACAGCCAG 122
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      129 CACCTGCAAGCCAGTCAGAGTGTAGTAATGATGTGGCTTGATCCACAGACAGCCAG 188
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      123 GCAGTCTCCGAATCTGTATATCTCTGCATCCATCGCTCACTGAGAGTCCCTGATCG 182
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Db 189 GCAATCTCTTAAGACATGATTTACTCGGACATCTTACCGGTACAGTGGAGTCCCTGATCG 248
Qy 183 CTTGACGTGGCAGTGGATATAGGACGAGATTTTCACTTTCACATCAGCACTGTGACGGCTGA 242
Db 249 CTTTACAGGAGAGTGGATCTGGGACAGATTTTCACTCTGACATCAGCAATGTGAGGTGCA 308
Qy 243 AGACCTGGCAGTTTATTTCTGTGACGACGAGATTATAGCT-----CGCTGGAGGGGG 293
Db 309 AGACTGGCAGAGATTTCTGTGACGACATATACAGCTATCCGCTCAAGTTGGTGTGCG 368
Qy 294 GACCAAGCTGGAATTAAGAGTGGAGGCGGTTTCAAGGCGGAGTGGCTGTGGCGGGCGG 353
Db 369 GACCAAGCTGAGATCAAGAGTGGTGGTGTGCTGGGCGGCGGCGCTCGGTGGTGGG 428
Qy 354 ATGCAAGTGGAGTGAAGAGTGAAGAGTGAAGAGTGGCTGGTGGCGGCTTCAAGAGCTGTG 413
Db 429 TTCTCAAGTGAATGCGAGAGTCAAGAGCTGGCTAGTGCAGCCCTTCAAGAGCTGTG 488
Qy 414 CATCACTTGCACGTCTGTGGGTTTCTTAAACCAATTATAGTGTACACTGGGTTCCCA 473
Db 489 CATCACTGCAAGTCTGTGGTTTCTTAACTAGCTATGTTGTACCTGGGTTCCCA 548
Qy 474 GCTTCCAGAAAGGCTGTGAGTGGCTGGAGTAAATATGGGCTGGTGAAGACAAATTA 533
Db 549 GTCTCCAGAAAGGCTGTGAGTGGCTGGAGTAAATATGGGCTGGTGAAGACAACTA 608
Qy 534 TAAATCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTTCAAGAGCCAAATTT 593
Db 609 TAAATGAGCTTTCATATCAGACTGAGCATCAGCAAGGACAACTTCAAGAGCCAAATTT 668
Qy 594 CTTTAAATGAAAGCTGTGCAAACTGATGACACAGCCATGTAATCTGTGCAAGTGGGG 653
Db 669 CTTTAAATGAAAGCTGTGCAAACTGATGACACAGCCATGTAATCTGTGCAAGTGG- 727
Qy 654 GGGTAACCTAGCGCTATGCTTGGACTATGAGTGGGTCAAGAACTTCAAGTCCGCTCC 711
Db 728 -----AGAACTGTGTGTTGCTTACTGGGGCCAAAGGACCAAGGTCACCGTCTCC 777

RESULT 7

LOCUS CO856167 1380 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 19 from Patent WO2004069876.
ACCESSION CO856167
VERSION CO856167.1 GI:51850992

KEYWORDS

SYNTHETIC CONSTRUCT

OTHER SEQUENCES; ARTIFICIAL SEQUENCES.

ORGANISM

REFERENCE 1 Kischel, R., Kufer, P., Lutterbuese, R., Offner, S. and Wolf, A.

AUTHORS

TITLE Enduring t cell response

JOURNAL

PATENT: WO 2004069876-A 19 19-AUG-2004;

FEATURES

SOURCE

Location/Qualifiers
1. .1380
/organism="synthetic construct"
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/note="scfv antiBpCAM-hu4-1BBL nucleic acid sequence"

ORIGIN

Query Match 66.6%; Score 475.2; DB 6; Length 1380;
Best Local Similarity 81.1%; Pred. No. 2.7e-115;
Matches 584; Conservative 0; Mismatches 118; Indels 18; Gaps 2;

Qy 3 TATGTGATGACCCAGATCTCCAAATTCCTGCTTATACAGACAGAGAGGTTACAT 62
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Qy 63 AACCTGCAAGGCGAGTCAAGTGTAGTAAAGATGTGCTGTGCTCAAGAGAGCCAG 122

Db 63 CACCTGCAAGGCGAGTCAAGTGTAGTAAATGTAGCTGTGATCAAGAAACCAG 122
Qy 123 GCACTTCCGAACTGCTGATATATCTGCATCCATTCGCTACCTGAGTCCCTGATCG 182
Db 123 GCAATCTCTTAAGACATGATTTACTCGGACATCTTACCGGTACAGTGGAGTCCCTGATCG 182
Qy 183 CTTGACGTGGCAGTGGATATAGGACGAGATTTTCACTTTCACATCAGCACTGTGACGGCTGA 242
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Qy 243 AGACCTGGCAGTTTATTTCTGTGACGAGATTATAGCT-----CGCTGGAGGGGG 293
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Qy 294 GACCAAGCTGGAATTAAGAGTGGAGGCGGTTTCAAGGCGGAGTGGCTGTGGCGGGCGG 353
Db 303 GACCAAGCTGAGATCAAGAGTGGTGGTGTGCTGGGCGGCGGCTCGGTGGTGGG 362
Qy 354 ATGCAAGTGGAGTGAAGAGTGAAGAGTGAAGAGTGGCTGGTGGCGGCTTCAAGAGCTGTG 413
Db 363 TTCTGATATCAAGCTGCAAGAGTGTGAACCTGGCTTGTGAGCCCTTCAAGAGCTGTG 422
Qy 414 CATCACTTGCACGTCTGTGGGTTTCTTAAACCAATTATAGTGTACACTGGGTTCCCA 473
Db 423 CATCACTGCAAGTCTGTGGTTTCTTAACTAGCTATGTTGTACCTGGGTTCCCA 482
Qy 474 GCTTCCAGAAAGGCTGTGAGTGGCTGGAGTAAATATGGGCTGGTGAAGACAAATTA 533
Db 483 GTCTCCAGAAAGGCTGTGAGTGGCTGGAGTAAATATGGGCTGGTGAAGACAACTA 542
Qy 534 TAAATCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTTCAAGAGCCAAATTT 593
Db 543 TAAATGAGCTTTCATATCAGACTGAGCATCAGCAAGGACAACTTCAAGAGCCAAATTT 602
Qy 594 CTTTAAATGAAAGCTGTGCAAACTGATGACACAGCCATGTAATCTGTGCAAGTGGGG 653
Db 603 CTTTAAATGAAAGCTGTGCAAACTGATGACACAGCCATGTAATCTGTGCAAGTGG- 661
Qy 654 GGGTAACCTAGCGCTATGCTTGGACTATGAGTGGGTCAAGAACTTCAAGTCCGCTCC 713
Db 662 -----AGAACTGTGTGTTGCTTACTGGGGCCAAAGGACCAAGGTCACCGTCTCC 713

RESULT 8

MUSVKLI

LOCUS

DEFINITION Mus musculus (clone H11) Ig kappa light chain V region (Vk), Ig heavy chain V region (Vh), and single chain Fv gene.

ACCESSION

VERSION L41689.1 GI:1119223

KEYWORDS

SOURCE

Mus musculus musculus (eastern European house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

COMMENT

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT


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Query Match 60.5%; Score 432; DB 10; Length 738;
Best Local Similarity 79.0%; Pred. No. 8,6e-104;
Matches 580; Conservative 0; Mismatches 115; Indels 39; Gaps 4;
QY 11 TGACCCAGACTCCCAATTCTGCTTATACAGACAGAGACAGGGTTACCAATCACTGCA 70
DB 14 TGACCCAGTCTCATCATCTCTGGCTGTGCTCAGGAGAAAAGTCATATAGAGCTGTA 73
QY 71 AGGCCAGTCAAGATGT-----GAGTAATGATGTGCTTGGTGTACCAAC 112
DB 74 AGTCCAGTCAAAAGTGTATTATACAGTCAAAATGAGAAAGTCTTGGCCTGGTACAGC 133
QY 113 AGAAGCAGGGGAGTCTCCGAAACTGCTATATATCTGCATCCATCGCTACACTGGAG 172
DB 134 AGAAACCAAGGAGCTCTCTAAGCTGTATCTACTGCGGATCACTAGGGAATCTGGTG 193
QY 173 TCCCTGATCGCTTCACTGGCAGTGAATATGGAAGGATTTCACTTACCATCAGACCTG 212
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DB 194 TCCCTGATCGCTTCACTGGCAGTGAATATGGAAGGATTTTACTTACCATCAGACCTG 253
QY 233 TGACCGTCAAGACTGCGAGTATTTCTGTACAGAGA---TTATAGTCTGCTGGAG 289
DB 254 TACACCTGAAGCTCGGAGAGTTTATCTGTATCAATACCTCTCCACACAGCTTGGAG 313
QY 290 GGGGACCAAGCTGGAATATAA-----GGTGAAGCGGTTGAGCGGAGTGGCT 340
DB 314 GGGGACCAAGCTGAGATCAAAACGTGTGACGCGGTGGGATCTGGTGGGGTGGCT 373
QY 341 CTGGCGGTGGCGGATGTCAGGTGACGTGAAGAGTCAAGACCTGCTGGTGGCCCT 400
DB 374 CCGCGGTGGCGGTTCTGTAAGTACAGCTTCAAGAGTCAAGACCTGCTGGTGGCCCT 433
QY 401 CACAGGCTGTCCATCACTGTGACCTGTGGTGTTCATTAACCAATTAATGAGTAC 460
DB 434 CACAGGCTGTCCATCACTGTGACCTGTGGTGTTCATTAACCAATTAATGAGTAC 493
QY 461 ACTGGTGGCGCAGCTCCAGGAAAGGTCGTGAGTGGAGTGAATATGAGCTGTG 520
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QY 521 GAAGCAAAATTAATTAATGCGCTTTATGTCCAGACTGACATCAGCAAGACACTCA 580
DB 554 GAAGCAAAATTAATTAATTAATGCGCTTTATGTCCAGACTGACATCAGCAAGACACTCA 613
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QY 641 GTGCCAGTGGGGGGGTAACTACGAGCTATGCTTTGAGTCACTGAGGTCAGGAACCTCAG 700
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QY 701 TCACCGTCTCTCA 714
DB 725 TCACCGTCTCTCA 738
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RESULT 9
LOCUS NM295476 840 bp mRNA linear ROD 29-OCT-1997
DEFINITION Mus musculus mRNA for IgM/kappa antibody, sefvus-CK.
ACCESSION 295476 AF004403
VERSION 295476.1 GI:2108308
KEYWORDS IGM.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 840)
AUTHORS Schouten,A., Roostien,J., de Boer,J.M., Wilmlink,A., Rosso,M.N.,
Bosch,D., Stiekema,W.J., Gommers,F.J., Bakker,V. and Schots,A.
TITLE Improving scFv antibody expression levels in the plant cytosol
JOURNAL FEBS Lett. 415 (2), 235-241 (1997)
MEDLINE 98010486
PubMed 9351003
REFERENCE 2 (bases 1 to 840)
AUTHORS Schouten,A.
DIRECT SUBMISSION Submitted (07-MAY-1997) Dept. of Nematology, Wageningen
Agricultural University, P.O. Box 8123, Wageningen 6700 BS, The
Netherlands
FEATURES
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PSLTSYGVHWKQSPGKLEWLVWGGVTVNAAPFMSRLSTIKDMSKSPFKMNS
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coding sequence"
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826..837
/note="KDEL coding sequence"

ORIGIN

Query Match 58.4%; Score 417.2; DB 10; Length 840;
Best Local Similarity 76.3%; Pred. No. 7.3e-100;
Matches 563; Conservative 0; Mismatches 148; Indels 27; Gaps 3;

QY 4 ATTGTGATGACCCAGACCTCCCAATTCCTGCTGTATACAGAGAGAGAGGTTACCTA 63
DB 22 ATTCAGATGACACAGTCTCCCACTCTGCTGTCTGAGAGAGAGAGGTTACCTA 81
QY 64 AACTGCAAGGCGAGTCAAGTGT-----GAGTAATGATGTGGCTTG 105
DB 82 AGCTGTAAGTCAAGTCAAGTGTGTATACAGTTCAATCAGAGAACTACTGGCTGG 141
QY 106 TACCAACAGAAACCAAGGCGAGTCTCCGAACCTGTGATATACCTGATCAATGCTAC 165
DB 142 TACCAGAGAAACCAAGGCGAGTCTCTTAACTGTGATCTAGGCTTCCACTAGAGAA 201
QY 166 ACTGAGTCCCTGATGCTGTACAGTGAAGTGAATGGAGAGATTTACCTTACCACTC 225
DB 202 TCCGATGCTCTGATGCTGTACAGGAGTGAATCTGGAGACAGATTTTAACTTACCACTC 261
QY 226 AGCAGTGCAGAGCTGTAAGACCTGCAATTTATTTCTGTACAGAGATTTATAGCTGC-- 283
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QY 284 ----TCGAGAGGAGGAGCCAGCTGGAATTAAGGTGAGCGGTTCAAGCGAGAGTGGC 339
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QY 340 TCTG---CGGATGCGGATTCGAGGTGAGTGAAGAGTCAAGACCTGGCTGTGGCG 396
DB 382 TCCCAATCCAAATCGAGTCTGAGGTGAATCTGGTGAATCTGAGCTGTAGTGAAG 441
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DB 442 CCCTCAAGAGCTGTGATCACTTCACTGCAAGTCTGTGGTTTCTATTAAGTACTAGT 501
QY 457 GTACACTGGGTTTGCAGAGCTTCAAGAAAGGCTGAGTGGCTGGAGTAAATGGGCT 516
DB 502 GTACACTGGGTTTGCAGAGCTTCAAGAAAGGCTGAGTGGCTGGAGTAAATGGAG 561
QY 517 GGTGAAAGCAAAATTAATTCGGCTTTATGTTCAGACTGAGATTAAGAGAGCAAC 576
DB 562 GGTGAAAGCAAGCTTAATGAGCTTTCAATGTTCAGACTGAGATTAAGAGAGCAAC 621
QY 577 TCCAAAGAGCAAGTTTCTTAATAATGAACAGTCTGCAACATGATGACAGAGCAATGAC 636
DB 622 TCCAAAGAGCAAGTTTCTTTAAATGAACAGTCTGCAAGCTGATGACAGTCCATATAC 681
QY 637 TACTGTGCAAGTCCGGGGGTTAATCAAGGCTATGCTTGTGACTATCGGGGTTCAAGAAC 696
DB 682 TACTGTGCAAAATTAATGATGTTAATCAAGGCTATGACTATGCGGTTCAAGAAC 741

QY 697 TCACTGACCGTCTCTCA 714
DB 742 TCACTGACAGTCTCTGCA 759
RESULT 10
AR481833
LOCUS AR481833 752 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 31 from patent US 6699715.
ACCESSION AR481833
VERSION AR481833.1 GI:47243499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 752)
AUTHORS Ledbetter,J.A., Hayden,M., Fell,P., Mitterler,R. and Winberg,G.
TITLE Modified sfv molecules which mediate adhesion between cells and
uses thereof
JOURNAL Patent: US 6699715-A 31 02-MAR-2004;
FEATURES
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ORIGIN

Query Match 58.0%; Score 414.4; DB 6; Length 752;
Best Local Similarity 76.9%; Pred. No. 4.1e-99;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

QY 4 ATTGTGATGACCCAGACCTCCCAATTCCTGCTGTATACAGAGAGAGAGGTTACCTA 63
DB 7 ATTGTGCTACCCCAATTCCTGCTGTATACAGTCTGTGCTGTGCTGTGCTGAGAGCCCACTC 66
QY 64 ACTGCAAGGCGAGTCAAGTGTGATGATGATGCT-----TGTACCAA 111
DB 67 TCTGAGAGAGCAAGTGAAGTGAATTAATGATCAAGTTTAATGAGAGTATACCA 126
QY 112 CAGAGCCAGGAGAGTCTCCGAACCTGTGATATCTGTGATCAATCGCTACACTGGA 171
DB 127 CAGAAACAGAGACGAGCCCACTCTCATCTGTGATCAATCAAGTGAATCTGG 186
QY 172 GTCCCTGATGCTTCACTGAGAGTGAATGAGAGGATTTCACTTACCATGAGCACT 231
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QY 232 GTGAGGCTGAAGACCTGGAGATTTATTTCTGTGAG-----AGATTATAGCTCG 282
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QY 283 CTGAGAGGAGGAGCAAGTGAATTAAG---GTGAGAGCGGTTCAAGCGAGTGGC 339
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QY 340 TCTGCGGCTGCGGATTCGAGTGCAGTGAAGAGTCAAGACCTGGCTGTGGCGCC 399
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QY 400 TCAAGAGAGCTGTGATCACTTGAATGCTGTGGGTTTTCATTAACCAATTAATGATG 459
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QY 460 CACTGAGTGTGAGCTTCAAGAGAGGCTGTGAGTGGCTGGAGTAAATGGGCTGT 519
DB 487 AACTGAGTGTGAGCTTCAAGAGAGGCTGTGAGTGGCTGGAGTAAATGATGAGGCTGAT 546
QY 520 GGAAGCAAAATTAATTCGGCTTTATGCTGATGCAAGTCAAGTCAAGAGCAAGCAATCC 579
DB 547 GGAAGCAAGCTTAATTAATGAGCTTCAAAATCAAGATGAGCAATCAAGAGCAATCC 606
QY 580 AAGAGCAAGTTTCTTAATAATGAACAGTCTGCAACATGATGACAGGCACTGATAC 639

Db 607 AAGACCAAGTTTCTTAAAAATGAACGCTGCAAACTGATGACAGCCAGACTAC 666
Qy 640 TGTGCCAGTGGGGGGGTAACACTAC-----GGCTATGCTTTGGACTTACGGGGTCAAGA 693
Db 667 TGTGCCAGAGATGTTATGTAACCTTTCATTACTATGATGACTCTGAGGCTCAAGA 726
Qy 694 ACCTCACTACCGTCTCTC 713
Db 727 ACCTCACTACCGTCTCTC 746

RESULT 11
AR481832
LOCUS AR481832 1509 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 30 from patent US 6699715.
ACCESSION AR481832
VERSION AR481832.1 GI:47243498
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1509)
AUTHORS Ledbetter, J.A., Hayden, M., Fell, P., Mittler, R. and Winberg, G.
TITLE Modified spy molecules which mediate adhesion between cells and uses thereof
JOURNAL Patent: US 6699715-A 30 02-MAR-2004;
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source Location/Qualifiers
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ORIGIN
Query Match 58.0%; Score 414.4; DB 6; Length 1509;
Best Local Similarity 76.9%; Pred. No. 3.9e-99;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

Qy 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATCAGCAGAGAGAGGTTACCAT 63
Db 1 ATTGTGCTCAACCAATCTCAGACTTCTTGGCTGTCTCTAGGTGACAGAGCCACCATC 60
Qy 64 ACCTGCAAGCCAGTCAAGTGTGATGATGATGCT-----TGGTACCA 111
Db 61 TCTGCGAGACCCAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 120
Qy 112 CAGAACGAGGGAGTGTCCGAAATGCTGATATGCTGATCCTCAATGCTACCTGCA 171
Db 121 CAGAACGAGAGACGACCAACCAATCTCTCATCTGCTGATCCTCAAGTGAATCTGG 180
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Qy 580 AAGAGCCAGTTTCTTAAAAATGAACAGTCTGCAAACTGATGACAGCCAGTACTAC 639
Db 601 AAGAGCCAGTTTCTTAAAAATGAACAGTCTGCAAACTGATGACAGCCAGTACTAC 660
Qy 640 TGTGCCAGTGGGGGGGTAACACTAC-----GGCTATGCTTTGGACTTACGGGGTCAAGA 693
Db 661 TGTGCCAGAGATGTTATGTAACCTTTCATTACTATGATGACTCTGAGGCTCAAGA 720
Qy 694 ACCTCACTACCGTCTCTC 713
Db 721 ACCTCACTACCGTCTCTC 740

RESULT 12
AR481831
LOCUS AR481831 1527 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 29 from patent US 6699715.
ACCESSION AR481831
VERSION AR481831.1 GI:47243497
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Ledbetter, J.A., Hayden, M., Fell, P., Mittler, R. and Winberg, G.
TITLE Modified spy molecules which mediate adhesion between cells and uses thereof
JOURNAL Patent: US 6699715-A 29 02-MAR-2004;
FEATURES
source Location/Qualifiers
1..1527
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/mol_type="genomic DNA"

ORIGIN
Query Match 58.0%; Score 414.4; DB 6; Length 1527;
Best Local Similarity 76.9%; Pred. No. 3.9e-99;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

Qy 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATCAGCAGAGAGAGGTTACCAT 63
Db 1 ATTGTGCTCAACCAATCTCAGACTTCTTGGCTGTCTCTAGGTGACAGAGCCACCATC 60
Qy 64 ACCTGCAAGCCAGTCAAGTGTGATGATGATGCT-----TGGTACCA 111
Db 61 TCTGCGAGACCCAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 120
Qy 112 CAGAACGAGGGAGTGTCCGAAATGCTGATATGCTGATCCTCAATGCTACCTGCA 171
Db 121 CAGAACGAGAGACGACCAACCAATCTCTCATCTGCTGATCCTCAAGTGAATCTGG 180
Qy 172 GTCCCTGATGCTTCACTGCGAGTGAATGAGACGATTTCACTTCAACATCAGCACT 231
Db 181 GTCCCTGCGAGTTTATGAGAGTGGGTCTGGAGCAGACTTCAGCCCTCAACATCTCAT 240
Qy 232 GTGCAAGCTGAAGACTGCGAGTTTATTTCTGTACG-----AGATTTATGCTCG 282
Db 241 GTGAGAGAGATGATATTTGCAATGATATTTCTGTCAAGCAAGTAGAAGGTTCTTGA 300
Qy 283 CTGCGAGGGGGGACCAAGCTGGAATTA---GTTGAGAGCGCTTCAAGCGAGGTGCG 339
Db 301 TTGCTGTGAGAGCAACCAAGCTGGAATTAACGGGGGTGCGGTGCGGTGCGGTGCG 360
Qy 340 TCTGCGAGTGGCGAGTGCAGGTGCAAGTGAAGAGTCAAGACCTGCGTGTGCGGCC 399
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Qy 400 TCACAGAGCTGTTCATCACTTGTGCACTGTCTGTGGTTTTCATTAAACCAATTATG 459
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Qy 460 CACTGGGTTCCGACGCTCCAGAAAGGGTGTGAGTGGCTGGAGTAAATGAGGCTGT 519
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Qy 520 GGAAGCAAAATTAATTCGGCTTTATGTCAGACTGAGCATCAGCAAGCAACTCC 579
Db 541 GGAAGCAAGACTTAATTCAGCTCTCAATTCAGACTGAGCATCAGCAAGCAACTCC 600
Qy 580 AAGAGCCAAAGTTTCTTAAATAAGAGCTGTGAAATCTGATGACAGAGCCATTAAC 639
Db 601 AAGAGCCAAAGTTTCTTAAATAAGAGCTGTGAAATCTGATGACAGAGCCATTAAC 660
Qy 640 TGTCCAGATCGGGGGGTAACACTAC-----GGCTATGCTTGGACTACTGAGGTCAGGA 693
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Qy 694 ACCTGAGTACCGTCTCTCTC 713
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RESULT 13

AR364987 729 bp DNA linear PAT 03-SEP-2003
LOCUS AR364987
DEFINITION Sequence 16 from patent US 5455030.
ACCESSION AR364987
VERSION AR364987.1 GI:34428209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 729)
AUTHORS Ladner,R.C., Bird,R.E. and Hardman,K.
TITLE Immunotherapy using single chain polypeptide binding molecules
JOURNAL Patent: US 5455030-A 16 03-OCT-1995;
FEATURES
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ORIGIN

Query Match 57.2%; Score 408.2; DB 6; Length 729;
Best Local Similarity 75.8%; Pred. No. 1.8e-97;
Matches 548; Conservative 0; Mismatches 163; Indels 12; Gaps 3;
Qy 4 ATTGTGATGACCCAGACTCCCAATTCCTGCTTATCAGCAGAGAGACAGGCTTACCA 63
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Qy 121 GGGGAGTCTCCGAAGTGTGATTAATCTGCATCAATGCTTACCTGAGAGTCCCTGAT 180
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Qy 241 GAAGACCTGCGAGTTTATTTCTGTCAAGAG-----GATTATAGTCTGCTGAGGGGG 294
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Qy 295 ACCAAGCTGGAATTAAGAGTGAAGCGGCTCAGGCGAGGCTGCTGCGGCTGCGGGA 354
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Qy 355 TCGCAGGTGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 414
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Db 727 TAA 729

RESULT 14

SYN507107 1632 bp RNA linear SYN 02-SEP-2002
LOCUS SYN507107
DEFINITION Synthetic construct for anti-CD28 and anti-HMWG ScFv antibody,
clone r28M.
ACCESSION AJ507107
VERSION AJ507107.1 GI:22759563
KEYWORDS antibody; heavy chain; immunoglobulin; light chain; ScFv; variable
region.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Grose-Hovest,L.
TITLE Produktion und Charakterisierung supra-agonistischer bispezifischer
CD28-Antikörper zur Tumor-Immuntherapie
JOURNAL Thesis (2002) Department of Biology, University of Tuebingen,
Tuebingen, Germany
2 (bases 1 to 1632)
REFERENCE Grose-Hovest,L.
AUTHORS Direct Submission
TITLE Submitted (28-AUG-2002) Grose-Hovest L., Membrane Biochemistry,
Max-Planck-Institute for Biochemistry, Am Klopferspitz 18a, 82152
Martinsried, GERMANY
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SOURCE

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ORIGIN

Query Match 57.1%; Score 407.8; DB 12; Length 1632;

Best Local Similarity 76.4%; Pred. No. 2.2e-97;
Matches 563; Conservative 0; Mismatches 147; Indels 27; Gaps 4;

QY 4 ATTGTGATGACCAAGTCTCCCAATTCCTGTTGATACAGAGAGACAGGTTACCAT 63
DB ATTGAGCTCACTAGTCTCAGCTCTTGGCTGTGCTCTAGAGCAGAGACCATCATC 120
QY 64 ACTGGAAGGCCGATGAGTGTGAATGATGTGCT-----TGGTACCA 111
DB TCTCGAGAGCCAGTGAAGTGTGAATGATGTGCAAGTTAATGACAGTGTACAG 180
QY 112 CAGAACCCAGGCGAGTCTCCGAAATGCTGATATACCTGATCCAAATGCTACATGGA 171
DB CAGAACCCAGGAGACGACCCAAATCTCTATCTTTGCTGATCCAAATGATGTGG 240
QY 172 GTCCCTGATGCTTCACTGCGAGTGAATGGAAGGATTTCACTTTCACCATCAGACT 231
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DB TTTCGAGGGGGGACCAAGCTGGAATTAATA---GTTGAGAGCGGTTCTGCGGTTGCGGA 420
QY 340 TCTGCGGTGGCGGATTCGAGGTGCAAGTGAAGAGTCAAGACCTGCGCTGTGCGGCC 399
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QY 520 GGAAGCAAAATTAATTTGGGCTCTTAATGCTCAAGTCAAGCAAGCAAACTCC 579
DB GGAGGACGAATTAATTTGGGCTCTCAATGCTCAAGAAAGCAATCAAGCAAACTCC 660

QY 580 AAGAGCAAGTTTCTTAATAAATGAACAGTCTGCAACTGATGACACAGCCATGTATAC 639
DB AAGAGCAAGTTTCTTAATAAATGAACAGTCTGCAACTGATGACACAGCCATGTATAC 720

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RESULT 15

AR481837 824 bp DNA linear PAT 14-MAY-2004

LOCUS AR481837 Sequence 38 from patent US 6699715.

DEFINITION AR481837

ACCESSION AR481837

VERSION AR481837.1 GI:47243503

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 824
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 56.1%; Score 400.2; DB 6; Length 824;

Best Local Similarity 76.4%; Pred. No. 2.4e-95;
Matches 572; Conservative 0; Mismatches 138; Indels 39; Gaps 5;

QY 4 ATTGTGATGACCAAGTCTCCCAATTCCTGTTGATACAGAGAGACAGGTTACCAT 63
DB ATTGAGCTCACTAGTCTCAGCTCTTGGCTGTGCTCTAGAGCAGAGACCATCATC 129
QY 64 ACTGGAAGGCCGATGAGTGTGAATGATGTGCT-----TGGTACCA 111
DB TCTCGAGAGCCAGTGAAGTGTGAATGATGTGCAAGTTAATGAGAGTGTACAG 189
QY 112 CAGAACCCAGGCGAGTCTCCGAAATGCTGATATACCTGATCCAAATGCTACATGGA 171
DB CAGAACCCAGGAGACGACCCAAATCTCTATCTTTGCTGATCCAAATGATGTGG 249
QY 190 CAGAACCCAGGAGACGACCCAAATCTCTATCTTTGCTGATCCAAATGATGTGG 249
DB GTCCCTGATGCTTCACTGCGAGTGAATGGAAGGATTTCACTTTCACCATCAGACT 231
QY 172 GTCCCTGATGCTTCACTGCGAGTGAATGGAAGGATTTCACTTTCACCATCAGACT 231
DB GTCCCTGCGAGTTAGTGGCAGTGGGTCTGGGACAAATTCAGCTCAACATCCATCT 309
QY 232 GTCCAGGCTGAACCTGCGAGTTATTCTGTCTCAG-----AGATTATAGCTCG 282
DB GTGGAAGAGGATATGTGCAATGTATTCTGTCTCAGCAAGTAGAAGGTTCTCTACAG 369
QY 283 CTCGAGGGGGGACCAAGCTGGAATTAATA---GTTGAGAGCGGTTCAAGCGGAGGTGCG 333
DB TTTCGAGGGGGGACCAAGCTGGAATTAATA---GTTGAGAGCGGTTCTGCGGTTGCGGA 429
QY 370 TCTGCGGTGGCGGATTCGAGGTGCAAGTGAAGAGTCAAGACCTGCGCTGTGCGGCC 459
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QY 388 CTGGTGGCCCTCACAAGAGCCGTGTCATCACTGCTGCTGCGTTTTCATTAAAC 447
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Db 670 AAAGACAACCTCCAAGAGCCAAATTTCTTAATAATGAAGAGTCTGCAAGCTGATGACACA 729
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QY 628 GCCATGTACTACTGTGCCAG--TCGGGGGGGTAACTACGGGCTATGCTTGGACTACTGG 684
|||
Db 730 GCCGTGTATTACTGTGCCAGAGATTAAGGATTAATCTCTATTAATACTATGACTACTGG 789
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QY 685 GGTCAAGGAACCTCAGTACCGTCTCCTC 713
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Db 790 GGTCAAGGAACCTCAGTACCGTCTCCTC 818
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 18:34:54 / Search time 418.122 Seconds
(Without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	714	100.0	714	6	ABA92027
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4	480	67.2	1479	12	ADQ91081
5	480	67.2	1479	12	ADQ91091
6	480	67.2	1479	12	ADQ91105
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25	408.4	57.2	729	2	AAQ51541	Aaq51541 Coding be
26	408.4	57.2	729	2	AAT13740	Aat13740 Single ch
27	408.4	57.2	729	2	AAT16464	Aat36464 18-2-3/TR
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33	398.4	55.8	720	2	AAT13739	Aat13739 Single ch
34	398.4	55.8	720	2	AAT36463	Aat36463 18-2-3/TR
35	398.2	55.8	727	2	AAT66143	Aat66143 PUR.4124
36	398.2	55.8	737	2	AAT94606	Aat94606 EcOR1-Hin
37	396.8	55.6	720	2	AAQ51540	Aaq51540 Coding be
38	396.2	55.5	728	2	AAQ70612	Aaq70612 I1-6 Bind
39	394.8	55.3	724	2	AAQ05714	Aaq05714 18-2-3-/T
40	393.2	55.1	739	2	AAQ78161	Aaq78161 PUR4125 V
41	383.2	53.7	1931	8	ABV73341	Abv73341 CD19:zeta
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45	365.6	51.2	1645	10	ADD25779	Add25779 Binding d

ALIGNMENTS

RESULT 1	
AA86310	
ID	AA86310 standard; DNA, 714 BP.
XX	
AC	AA86310;
XX	
DT	06-APR-1998 (first entry)
XX	
DE	Single chain anti-disialoganglioside GD2 antibody 3G6-scfv.
XX	
KW	Antibody construct; disialoganglioside; GD2; single chain Fv fragment;
KW	scfv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;
KW	tissue imaging; target delivery; toxin; streptavidin;
KW	pro-drug converting enzyme; GD2-targeted lymphocyte; ss.
XX	
OS	Synthetic.
XX	
FN	WO9734634-A1.
XX	
PD	25-SEP-1997.
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PF	20-MAR-1997; 97WO-US004427.
XX	
PR	20-MAR-1996; 96US-0013703P.
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PA	(SLOK) SLOAN KETTERING INST CANCER RES.
XX	
PI	Cheung NV, Larson SM, Guo H, Rivlin K, Sadelain M,
XX	WPI; 1997-47996/44.
DR	
XX	
PT	Recombinant single chain anti-disialoganglioside GD2 antibody - useful to
PT	detect tumour cells expressing GD2 and to target therapeutic agents, e.g.
PT	toxins, to such cells.
XX	
PS	Disclosure; Page 11-12; 31p; English.
XX	
CC	The present sequence encodes a recombinant single chain peptide, 3G6-
CC	scfv. The peptide is an antibody construct comprising the variable
CC	regions of the heavy and light chains of an antibody against
CC	disialoganglioside (GD2) as a single chain Fv fragment (scfv). GD2 occurs
CC	in many tumour types including neuroblastoma, osteosarcoma and other
CC	soft tissue sarcomas, medulloblastomas, high grade astrocytomas,

Accession	Gene	Protein	Accession	Gene	Protein
QY	CTGGAATAAAGGTCGAGACCGGTTTCAGGCGAGAGTGCTCTCGGCGGTGGCCGATGCGAC	360	QY	CTGGAATAAAGGTCGAGACCGGTTTCAGGCGAGAGTGCTCTCGGCGGTGGCCGATGCGAC	360
Db	301 CTGGAATAAAGGTCGAGACCGGTTTCAGGCGAGAGTGCTCTCGGCGGTGGCCGATGCGAC	360	Db	301 CTGGAATAAAGGTCGAGACCGGTTTCAGGCGAGAGTGCTCTCGGCGGTGGCCGATGCGAC	360
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Db	421 TCGACATGCTCTGGGTTTTCATTAACCAATTATGTGTACACTGGGTTGGCCAGCTCCA	480	Db	421 TCGACATGCTCTGGGTTTTCATTAACCAATTATGTGTACACTGGGTTGGCCAGCTCCA	480
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Db	481 GGAAGAGGCTCTGGAGTGGCTGGGAGTAAATATGTGGCTGTGTGAAGCAAAATTAAATTGG	540	Db	481 GGAAGAGGCTCTGGAGTGGCTGGGAGTAAATATGTGGCTGTGTGAAGCAAAATTAAATTGG	540
QY	GCTCTTATGTCCAGACTGAGCTGAGCAAGGACCAATCCAGAGCCAAAGTTTCTTAAAA	600	QY	GCTCTTATGTCCAGACTGAGCTGAGCAAGGACCAATCCAGAGCCAAAGTTTCTTAAAA	600
Db	541 GCTCTTATGTCCAGACTGAGCTGAGCAAGGACCAATCCAGAGCCAAAGTTTCTTAAAA	600	Db	541 GCTCTTATGTCCAGACTGAGCTGAGCAAGGACCAATCCAGAGCCAAAGTTTCTTAAAA	600
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Db	601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGTGTCCAGTGGGGGGGTAAAC	660	Db	601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGTGTCCAGTGGGGGGGTAAAC	660
QY	TACGGCTATGCTTTGGACTACTGTGGGGTCAAGAACTCAAGTCAACCGTCTCTCTCA	714	QY	TACGGCTATGCTTTGGACTACTGTGGGGTCAAGAACTCAAGTCAACCGTCTCTCTCTCA	714
Db	661 TACGGCTATGCTTTGGACTACTGTGGGGTCAAGAACTCAAGTCAACCGTCTCTCTCTCA	714	Db	661 TACGGCTATGCTTTGGACTACTGTGGGGTCAAGAACTCAAGTCAACCGTCTCTCTCTCA	714

PT									t toxins, to such cells.
XX									
PS									
XX									Diclosureure; Page 13; 31pp; English.
CC									The present sequence encodes a recombinant single chain peptide, 3G6-scFv
CC									-streptavidin. The peptide is an antibody construct comprising the
CC									variable regions of the heavy and light chains of an antibody against
CC									dihaloganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
CC									in many tumour types including neuroblastoma, osteosarcomas and other
CC									soft tissue sarcomas, medulloblastomas, high grade astrocytomas,
CC									melanomas and small cell lung cancer. The peptide can be detectably
CC									labelled, preferably with ^{99m} Tc, for tissue imaging of cells expressing
CC									GD2. It can also be used to target delivery of a therapeutic or pre-
CC									therapeutic agent, such as a toxin, streptavidin (e.g. present sequence)
CC									or a pro-drug converting enzyme, to cells expressing GD2. The peptide may
CC									further comprise CD8 to facilitate the formation of GD2-targeted
CC									lymphocytes. T cells containing the peptide can also be used to target
SQ									
	Sequence	1173 BP;	270 A;	334 C;	340 G;	229 T;	0 U;	0 Other;	
	Query Match		100.0%;	Score 714;	DB 2;	Length 1173;			
	Beet Local Similarity		100.0%;	Pred. NO. 8,1e-198;					
	Matches 714;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

OY	1	AGTATTGGATGAGACCCAGACCTCCAAATTCCTGCTGTGATATCAGACAGGAGACAGGGTTAC	60
OY	1	AGTATTGGATGAGACCCAGACCTCCAAATTCCTGCTGTGATATCAGACAGGAGACAGGGTTAC	60
OY	61	ATTAACCTGCAGAGGCGCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTATCCACAGAAAGCCA	120
Db	61	ATTAACCTGCAGAGGCGCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTATCCACAGAAAGCCA	120
OY	121	GGGCAGTTCCTCGAAAACCTGCTGATATATCTCTGCATCCAAATGGCTACACTGGAAGTCCCTGAT	180
Db	121	GGGCAGTTCCTCGAAAACCTGCTGATATATCTCTGCATCCAAATGGCTACACTGGAAGTCCCTGAT	180
OY	181	CGCTTCACTGGCAGTGGATATGGGACGGATTTTCACCTTCAACATCAGACACTGTGCAGGCT	240
Db	181	CGCTTCACTGGCAGTGGATATGGGACGGATTTTCACCTTCAACATCAGACACTGTGCAGGCT	240
OY	241	GAAGACCTGGCAGTTATTTTCTGTCAAGCAGGATTATAGCTGCTTCGAGGGGGGACCAAG	300
Db	241	GAAGACCTGGCAGTTATTTTCTGTCAAGCAGGATTATAGCTGCTTCGAGGGGGGACCAAG	300
OY	301	CTGGAAATATAAAGGTGAGAGCGGCTTCAAGGCGGAGGTGGCTTGGCGGTGGCGATTCGAG	360
Db	301	CTGGAAATATAAAGGTGAGAGCGGCTTCAAGGCGGAGGTGGCTTGGCGGTGGCGATTCGAG	360
OY	361	GTGACAGGTGAAGAGAGTCAGACCTGGGCTGGTGGGCGCCCTCACAAGACCTGTCCATCACT	420
Db	361	GTGACAGGTGAAGAGAGTCAGACCTGGGCTGGTGGGCGCCCTCACAAGACCTGTCCATCACT	420
OY	421	TGCATGTCTCTGGGGTTTTCATTAACCAATTATGATGTACACTGGGTTTCGCGCAGCTTCCA	480
Db	421	TGCATGTCTCTGGGGTTTTCATTAACCAATTATGATGTGTACACTGGGTTTCGCGCAGCTTCCA	480
OY	481	GGAAGAGGTCCTGAGAGTGGCTGGAGATATATGGGCTGGTGGAAACACAATAATTAAATTCG	540
Db	481	GGAAGAGGTCCTGAGAGTGGCTGGAGATATATGGGCTGGTGGAAACACAATAATTAAATTCG	540
OY	541	GCTCTTATGTCCAGACTGAGCATCAGACAGGACAACATCCAAAGGCAAGTTTCTTAAAA	600
Db	541	GCTCTTATGTCCAGACTGAGCATCAGACAGGACAACATCCAAAGGCAAGTTTCTTAAAA	600
OY	601	ATGAACAGTCTGCAGAACTGATGACACAGCCATGTACTATCTGTGCCAGTCTGGGGGGGTAC	660
Db	601	ATGAACAGTCTGCAGAACTGATGACACAGCCATGTACTATCTGTGCCAGTCTGGGGGGGTAC	660
OY	661	TACGGCTATGCTTTGGAATACTGGGGGTCAAGAAACCTCAGTCAACGCTCTCTCA	714
Db	661	TACGGCTATGCTTTGGAATACTGGGGGTCAAGAAACCTCAGTCAACGCTCTCTCA	714

ID	ADQ91081	standard; DNA; 1479 BP.
XX	ADQ91081;	
XX	23-SEP-2004	(first entry)
DE	Antibody scFv EpcAMKCD3 with M1 mutant in anti CD3 region encoding DNA.	
XX	CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;	
KW	immunosuppressive; proliferative disease; tumour; inflammatory disease;	
KM	immunological disorder; autoimmune disease; infectious disease;	
KW	scFv EpcAMKCD3; antibody; ds.	
OS	Synthetic.	
OS	Unidentified.	
Key	Location/Qualifiers	
FD	1..1479	
FT	/tag=a	
FT	/product="scFv EpcAMKCD3 with M1 mutant in anti CD3	
FT	region"	
FT	/note="No start codon"	
XX	CA2403313-A1.	
XX	11-APR-2004.	
XX	11-OCT-2002; 2002CA-02403313.	
XX	11-OCT-2002; 2002CA-02403313.	
XX	(MICR-) MICROMET AG.	
PI	Lanzavecchia A;	
DR	WPI; 2004-390792/37.	
DR	P-PSDB; ADQ91080.	
PT	Antibody construct, useful in treating, e.g., cancer and inflammatory	
PT	diseases comprises at least one mutated CDR3 region.	
PS	Claim 22; SEQ ID NO 62; 80pp; English.	
XX	The invention relates to a novel polypeptide construct comprising at	
CC	least one CDR3 region comprising at least one mutation in a fully defined	
CC	sequence of 6 amino acids. A construct of the invention has	
CC	antiinflammatory, antimicrobial, cytostatic, immunomodulator, and	
CC	immunosuppressive activity. The polypeptide construct, polynucleotide,	
CC	vector or composition are useful for the prevention, treatment or	
CC	amelioration of a proliferative disease, a tumorous disease, an	
CC	inflammatory disease, an immunological disorder, an autoimmune disease or	
CC	bi-specific single chain antibody scFv EpcAMKCD3 with the M1 mutant	
CC	peptide in the anti CD3 region.	
XX	Sequence 1479 BP; 385 A; 365 C; 389 G; 340 T; 0 U; 0 Other;	
QY	Query Match	67.2%; Score 480; DB 12; Length 1479;
Db	Best Local Similarity	81.5%; Pred. No. 1.9e-129;
Db	Matches 587; Conservative	0; Mismatches 115; Indels 18; Gaps 2
QY	3 TATTGTGATGACCCAGACTCCCAATTCTCTGTTGATACAGAGAGAGAGGTTACAT	62
Db	3 TATTCAGCTGACCCAGCTCCAAAATTCATGTCCACATCAGTAGAGAGACAGGCTCAGCGT	62
QY	63 AACCTGCAAGGCGACATGAGAGTGTATATATGTGCTTGATCCAAACAGAGCGAG	122
Db	63 CACCTGCAAGGCGACATGAGAGTGTGTGATATATGTAGCTGTATCAACAGAAACGAG	122
QY	123 GCAGTCTCCGAAACTGCTGATATATCTGTGATCCAAATGCTACACTGAGTCCCTGATCG	182

Dd			123 GCATCTCCTAAAGCACTGATTATTCCTGGCATCTCTACCGGTGACGTGAATCCCTATCG	182
Oy			183 CTTCACTGCGAGTGGAATATGGACGCAGATTTCATTCCATCAGACACTGACAGCTGA	242
Dd			183 CTTCAcAGGcAGTGGATCTGGGAcAGATTTCACtCTcAGcATcAGCAAtGtGcAGtCTGA	242
Oy			243 AGAcCTGCGAcTTTAATTTCTGTcGAcGAGAATTATAgCT-----CGCTGGAGGGGG	293
Dd			243 AGAcTTGGGAcGATTAATTTCTGTcGAcCAATAATAAcGCTATTCGCTCAcGTTCCGTTGTGG	302
Oy			294 GACCAAGCTGSAATATAAAGGTGGAGGGCGTTTCAGGCCGAGAGTGGCTCTGGCGGTGGCGG	353
Dd			303 GACCAAGCTCGAGATCAAAAGTGTGTGTGTCTTGGCGGCGGCGGCTCCGGTGTGTGG	362
Oy			354 ATGCAAGGTGCAAGGTGAAGAGTCAAGAcCTTGCCCTGTGTGGCGCCCTCACAGACCCTGTc	413
Dd			363 TTCTCAGGTGAAAcCTGcAGAGAGTcAGAGcCTTGCCCTATGTGAcGCCCTCACAGAGCCTGTc	422
Oy			414 CATCACTTGOAcTGTCTCTGGGTTTTCAATTAACAATTATGTGTACACTGGGTTGGCCA	473
Dd			423 CATCACTTCAcAGTCTCTGTGTTTTCTCAATTAAGTATATGTGTACAcTGGGTTCCCCA	482
Oy			474 GCCTCCAGAAAGGGCTCGAGcTGGcCTGGGAGTAATAGGCGTGGTGGAGCAAAATTA	533
Dd			483 GTCTCCAGAAAGGGCTCGAGTGGCTGGAGTGAATAGGTGTGAAGCAcAGACTA	542
Oy			534 TAATTCGGCTCTTAATGTCcAGAcTGAAGATCAGAcAGACAACTCCAAAGACCAAGTTTT	593
Dd			543 TAATGAcGTTTTCAATTCcAGcTGAAGATcAGCAAGSAGCAATTCcAAAGSCCAAGTTTT	602
Oy			594 CTTAAAAATGAACAAGTCTGCAAACGTATGACAcAGCCATGTACTACTGTGCGACGTGGGG	653
Dd			603 CTTAAAAATGAACAAGTCTGCAAAGTAAATGAACAAGCAATATATTACTGTGCCAATATGG-	661
Oy			654 GGGTAACTAGGGCTATGCTTTGGACTATCGGGGTCAAGSAACTCCAGTCAcCGTCTCTC	713
Dd			662 -----GAAAcTGGTGTGTGCTTACTTcGGGCGAAAGSACAcAGGTCAcCGTCTCTCTC	713

RESULT 5	
ID	ADQ91091 standard; DNA; 1479 BP.
XX AC	ADQ91091;
XX DT	23-SEP-2004 (first entry)
DE DB	Antibody scFv EpcAMKCD3 with M1 mutant in anti CD3 region encoding DNA.
XX KW	CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW KW	immunosuppressive; proliferative disease; tumour; inflammatory disease;
KW KW	immunological disorder; autoimmune diseasee; infectious diseasee;
KX KW	scFv EpcAMKCD3; antibody; ds.
XX OS	Synthetic.
OS OS	Undentified.
FT FT	Key
FT FT	CDS
FT FT	Location/Qualifiers
FT FT	1..1479
FT FT	/tag= a
FT FT	/product= "scFv EpcAMKCD3 with M1 mutant in anti CD3
FT FT	region"
FT FT	/note= "No start codon"
FT FT	/transl_except= (pos:625..627,aaAla)
XX PN	CA2403313-AI.
XX PD	11-APR-2004.
XX PE	11-OCT-2002; 2002CA-02403313.
XX PR	11-OCT-2002; 2002CA-02403313.

XX (MICR-) MICROMET AG.
PA
XX Lanzavecchia A;
PI
XX WPI: 2004-390792/37.
DR P-PSDB; ADQ91090.
XX
PT Antibody construct, useful in treating, e.g., cancer and inflammatory
PT diseases comprises at least one mutated CDR3 region.
XX
PS Claim 22; SEQ ID NO 72; 80bp; English.
XX
CC The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined
CC sequence of 6 amino acids. A construct of the invention has
CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
CC immunosuppressive activity. The polypeptide construct, polynucleotide,
CC vector or composition are useful for the prevention, treatment or
CC amelioration of a proliferative disease, a tumorous disease, an
CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence encodes
CC bispecific single chain antibody scFv EpCAMxCD3 with the M11 mutant
CC peptide in the anti CD3 region.
XX
SQ Sequence 1479 BP; 385 A; 365 C; 387 G; 342 T; 0 U; 0 Other;
Query Match 67.2%; Score 480; DB 12; Length 1479;
Best Local Similarity 81.5%; Pred. No. 1.9e-129;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
QY 3 TATGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGACGAGACAGGGTTACAT 62
DB 3 TATCCACCTGACCCAGCTCAAAATTCATGTCCACATCAGTAGAGCAGGGTACAGCGT 62
QY 63 AACCTGCAAGGCCAGTGAAGTGAATGATGATGCTGGCTGTACCAAGAGACCG 122
DB 63 CACCTGCAAGGCCAGTGAAGTGAATGATGATGCTGGCTGTACCAAGAGACCG 122
QY 123 GCACTCTCCGAACTGATATATCTGATTCATCCATGCTACATGAGTCCCTGATCG 182
DB 123 GCAATCTCTTAAACACTGATTTACTCGGCATCCCTACCGGTACAGTGGAGTCCCTGATCG 182
QY 183 CTTCACCTGGCAGTGAATGAGGAGATTTCACTTTCACCTACAGCTGCGGCTTGA 242
DB 183 CTTCACCTGGCAGTGAATGAGGAGATTTCACTTTCACCTACAGCTGCGGCTTGA 242
QY 243 AGACCTGGCAGTGAATGAGGAGATTTCTGTCAGCAGATTTAGCT-----CGCTCGAGGGGG 293
DB 243 AGACCTGGCAGTGAATGAGGAGATTTCTGTCAGCAGATTTAGCTCGCTCGAGGGGG 302
QY 294 GACCAAGCTGGAATTAAGAGTGAAGCGGTTTCAGGCGGAGGTGGCTTGGCGGTGGCG 353
DB 303 GACCAAGCTGGAATTAAGAGTGAAGCGGTTTCAGGCGGAGGTGGCTTGGCGGTGGCG 362
QY 354 ATGCGCAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 413
DB 363 TTCTCAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 422
QY 414 CATACCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 473
DB 423 CATACCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 482
QY 474 GCTTCAGGAAGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 533
DB 483 GCTTCAGGAAGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 542
QY 534 TAAATCGGCTTTATGTCAGACTGAGATCAGCAAGCAATCCCAAGACCAAGTTT 593
DB 543 TAAATCGGCTTTATGTCAGACTGAGATCAGCAAGCAATCCCAAGACCAAGTTT 602
QY 594 CTTAAATGAAAGTGTGCAAACTGATGACAGACCATGACTGACTGCTGCGAGTGGGG 653

DB 603 CTTAAATGAAAGTGTGCAAACTGATGACAGACCATATATGATGCTGCGAGATG- 661
QY 654 GGGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 713
DB 662 -----AGAACTGTGCTTGTCTTACTGGGGCAAGGACACCGGTACCGTCTCTC 713
RESULT 6
ADQ91105
ID ADQ91105 standard; DNA; 1479 BP.
XX
XX ADQ91105;
XX
XX 23-SEP-2004 (first entry)
XX
XX Antibody scFv EpCAMxCD3 with M69 mutant in anti CD3 region encoding DNA.
XX
XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
XX immunosuppressive; proliferative disease; tumour; inflammatory disease;
XX immunological disorder; autoimmune disease; infectious disease;
XX scFv EpCAMxCD3; antibody; ds.
XX
XX Synthetic.
XX Undetected.
XX
XX Key Location/Qualifiers
FT CDS 1..1479
FT /*tag= a
FT /product= "scFv EpCAMxCD3 with M69 mutant in anti CD3
FT region"
FT /note= "No start codon"
FT /transl_except= (pos:1054..1056,aa:Tyr)
XX
XX CA2403313-A1.
XX
XX 11-APR-2004.
XX
XX 11-OCT-2002; 2002CA-02403313.
XX
XX 11-OCT-2002; 2002CA-02403313.
XX
XX (MICR-) MICROMET AG.
XX
XX Lanzavecchia A;
XX
XX WPI: 2004-390792/37.
XX P-PSDB; ADQ91104.
XX
XX Antibody construct, useful in treating, e.g., cancer and inflammatory
XX diseases comprises at least one mutated CDR3 region.
XX
XX Claim 22; SEQ ID NO 86; 80bp; English.
XX
XX The invention relates to a novel polypeptide construct comprising at
XX least one CDR3 region comprising at least one mutation in a fully defined
XX sequence of 6 amino acids. A construct of the invention has
XX antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
XX immunosuppressive activity. The polypeptide construct, polynucleotide,
XX vector or composition are useful for the prevention, treatment or
XX amelioration of a proliferative disease, a tumorous disease, an
XX inflammatory disease, an immunological disorder, an autoimmune disease or
XX an infectious disease in a human subject. The present sequence encodes
XX bispecific single chain antibody scFv EpCAMxCD3 with the M69 mutant
XX peptide in the anti CD3 region.
XX
SQ Sequence 1479 BP; 387 A; 364 C; 389 G; 339 T; 0 U; 0 Other;
Query Match 67.2%; Score 480; DB 12; Length 1479;
Best Local Similarity 81.5%; Pred. No. 1.9e-129;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
QY 3 TATGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGACGAGACAGGGTTACAT 62

Db	3	TATCCAGCTGACCCAGAGCTCAAAAATTCTATGTCACATCAGTAGGAGACAGGGTCAAGGT	62
Oy	63	AACCTGCAAGCCAGTCAGAGTGTGATGATATATGTGGCTTGTAACCAACGAAGCCAGG	1222
Db	63	CACCTGCAAGGCCAGTCAGATGTGGGATCTATATGTACCTGTGATCAACGAAACCAAGG	1222
Oy	123	GCAGTCTCCGAAACTGTCTATATCTGTGCATCCATGCTGACACTGAGAGTCCCTGATCG	1828
Db	123	GCATCTCTTAAGCACTGATTTATCTCGGCATCTCAACGGATCAGGTGAGTCCCTGATCG	1828
Oy	183	CTTTCACGTGCGATGGAATATGGGACGGATTTCCTTCAACATCAGACCTGTGCAGCTGA	2424
Db	183	CTTTCACAGGCGATGGATCTGGGACAGATTTCCTCAACATCAGCAATGTGCGAGTCTGA	2424
Oy	243	AGACCTGGACGTTTATTTCTGTGACGAGGATTAATAGCT-----CGCTCGAAGGGGG	2993
Db	243	AGACTTGGACAGATATTTCTGTGACCAATATTAACAGCTATCCGCTCAGTTCGGGTCTGG	3020
Oy	294	GACCAAGCTGGAAATATAAAGGTGAGGCGGTTCAAGGCGAGAGTGCTCTGGCGGTGGCG	3533
Db	303	GACCAAGCTGAGATCAAAAGTGATGTGTGTTCTGGCGGCGGGCTCGGTTGGTGGTG	3626
Oy	354	ATGTCAGGTGCGAGTGAAGAGTCAGGACTTGGCTGTGGCGCTTCAACAGACCTGTCTC	4133
Db	363	TTTTCAGGTGAAACTCAGAGAGTCAGGACCTTGAGCCCTCAACAGACCTGTCTC	4222
Oy	414	CATCACTTGCACTGTCTGTGGTTTTCAATTAACAATATGATGTGACACTGGGTTTCGCA	4733
Db	423	CATCACTTGCAAGTCTGTGGTTTTCTCAATTAACATGCTATGATGTGACCTGGGTTTCGCA	4826
Oy	474	GCTTCAGGAAGGTTCTGAGTGGCTGGGAGTAATATGGCGTGTGGAGCACAAAATTA	5333
Db	483	GTCTCCAGGAAGGTTCTGAGTGGCTGGGAGTAATATGGCGTGTGGAGCAACAGACTA	5426
Oy	534	TAAATTGGGCTCTAATGCCAGACTGAGGATCAGCAAGGACAACTCAAGAGCCAAAGTTT	5933
Db	543	TAAATGAGCTTTCAATTCAGACTGAGCATCAGCAAGGACAAATTTCCAGAGCCAAAGTTT	6026
Oy	594	CTTAAATAATGACAGTCTGCAAACTGATGACACAGCCATGTACTATCTGTGCCAGTGGGG	6533
Db	603	CTTAAATAATGACAGTCTGCAAGCTAATGACACAGCCATATATTACTGTGCCAATATGG-	6616
Oy	654	GGGTAATACGGCTATGCTTTGGACTACTGGGGGTCAAGAACTTCAGTCAACCGTCTCTC	7133
Db	662	-----AATACTGATCGTTGTCTTACTCTGGGGCCAGAGGACACACGATCAACCGTCTCTC	7133

RESULT 7
ADQ91079
ID ADQ91079 standard; DNA; 1479 BP.
XX
AC ADQ91079;
XX
DT 23-SEP-2004 (first entry)
XX
DE Bisppecific single chain antibody scFv EPCAMxCD3 SEQ ID NO:60.
XX
KM CD3; antiinflammatory; antimicrobial; cytostatic; immunomodulator; KM immunosuppressive; proliferative disease; tumour; inflammatory disease; KW immunological disorder; autoimmune disease; infectious disease; KW scFv EPCAMxCD3; antibody; ds. XX
OS Synthetic. OS Undentified. XX
FH Key FH CDS
XX
FT Location/Qualifiers FT 1..1479 FT /*tag= a FT /product= "scFv EPCAMxCD3" FT /note= "No start codon given"
XX
PN CA2403313-A1. XX

PD	11-APR-2004.
XX	
PF	11-OCT-2002; 2002CA-02403313.
XX	
PR	11-OCT-2002; 2002CA-02403313.
XX	
PA	(MICR-) MICROMET AG.
XX	
PI	Lanzavecchia A;
XX	
DR	WPI; 2004-390792/37.
DR	P-PSDB; ADQ91078.
XX	
PT	Antibody construct, useful in treating, e.g., cancer and inflammatory diseases comprises at least one mutated CDR3 region.
XX	
PS	Example 7; SEQ ID NO 60; 80pp; English.
XX	
CC	The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defined sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease or an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv BpCmxC03.
XX	
XX	Sequence 1479 BP; 385 A; 364 C; 389 G; 341 T; 0 U; 0 Other;

Query Match	67.2%;	Score 480;	DB 12;	Length 1479;
Best Local Similarity	81.5%;	Pred. No. 1,9e-129;		
Matches 587;	Conservative 0;	Mismatches 115;	Indels 18;	Gaps 2;
QY	3	TAATGTGATGATCCACAGCTCCCAATTCCTCGTTGTATACAGCAGAGACAGGGTTACCAT	62	
Db	3	TATTCAGCTTACCCACAGCTCTCAAAAATTCATGTCACATCAGTAGAGACAGGGGTCAAGCT	62	
QY	63	AACCTGCAAGGCCAGTACAGATGTGAGTAATGATGTGGCTTGGTACCAACAGAACGACAG	122	
Db	63	CACCTGCAAGGCCAGTACAGATGTGGGTACTAATGTATGCTGTGGTATACAGAAACGAG	122	
QY	123	GCACTCTCCGAAACTGCTGATATATCTGTGATCCATATGCTACATCTGGAATCCTGATTCG	182	
Db	123	GCAATCTCCGAAAGCACTGATTTAATCTGGGATCTTACCGGTACAGTGAAGTCCCTGATTCG	182	
QY	183	CTTCACATGGCAGTGGATATGAGACGAGATTCACATTACACATCAGCACTGTGCAGGCTGA	242	
Db	183	CTTTCACAGGAGATGATCTGGGACAGATTTCACTCTCAATCAGCAATGTGCAGTCTGA	242	
QY	243	AGACTGGCAGTTAATTTCTGTGCAGCAGATTATAGCT-----CGCTCGAGGAGGG	293	
Db	243	AGACTGGCAGAGATTAATTTCTGTGCAGCAATATTAACAGTATACCGCTCACTGTTGGTGTGG	302	
QY	294	GACCAACCTGGAATTAATAGTGAAGCGGTTTCAAGCGGAGTGGCTCTGGCGGTGGCGG	353	
Db	303	GACCAACCTGAGATCAAAAGTGTGTGTCTTGGCGGCGGCGGCTCCGGTGTGGTGG	362	
QY	354	ATCGCAGGTGCAGTGAAGAGTCAAGACCTGGCTGTGGCGGCTTCACAGAGCCTGTCT	413	
Db	363	TTCTCAGGTGAATCTGAGAGTCAAGGACCTGGGCTTGTAGTCAAGCCCTCACAGAGCTGTCT	422	
QY	414	CATCATCTTGACATGTCTCTGGGTTTTATTAACAATTAATAGTGTAAACTGTGGTTCCCA	473	
Db	423	CATCATCTTGACAGTCTCTGTGTTCTATTAACTAGTAATGTGTAACTGTGGTTCCCA	482	
QY	474	GCTCCAGAAAGGGTCTGAGTGGCTGGGAGTAAATGTGGCTGTGGAGCAAAAATTA	533	
Db	483	GTCCTCAGAAAGGGTCTGAGTGGCTGGGAGTAAATGTAGTGTGGAAAGCAAGACTA	542	
QY	534	TAATTCGGCTTATATGTCCAGCTGAGCATCAGCAGGACAACTCCAAAGGCCAAGTTT	593	

Db 543 TAATGACCTTTCATATCCAGACTGAGCATCAGCAAGGCAATTCCAAGAGCAAGTTT 602
QY 594 CTTAAAAATGAACTGTGCAAACTGATGACACAGCCATGTACTCTGCGCAAGTGGG 653
Db 603 CTTAAAAATGAACTGTGCAAGCTAAATGACACAGCCATATATTACTGTGCGAGATG- 661
QY 654 GGGTAACTACGCTATGCTTTGGAATCACTAGGGGTCAAGAACTCAGTCACCGTCTCTC 713
Db 662 -----AGAACTGTGCTTTGCTTACTGCGGCGCAAGGACCAAGTCACCGTCTCTC 713

RESULT 8
ADS99440
ID ADS99440 standard; DNA; 1479 BP.
AC ADS99440;
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Antibody scFv EpcAMxCD3 with M13 mutant in anti CD3 region encoding DNA.
DE
XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
KW immunological disorder; autoimmune disease; infectious disease;
KW scFv EpcAMxCD3; antibody; ds.
XX
OS Synthetic.
OS Unidentified.

XX
FH Key Location/Qualifiers
FT 1.1479
FT CDS /tag= a
FT /product= "scFv EpcAMxCD3 with M13 mutant in anti CD3
FT region"
FT /note= "No start codon"

XX CA2403313-A1.
PN
XX
XX 11-APR-2004.
PD
XX
XX 11-OCT-2002; 2002CA-02403313.
PE
XX 11-OCT-2002; 2002CA-02403313.
PR
XX 11-OCT-2002; 2002CA-02403313.
XX
PA (MICR-) MICROMET AG.
XX
XX Lanzavecchia A;
PI
XX WPI; 2004-390792/37.
DR
DR P-PSDB; ADS99439.
XX
XX Antibody construct, useful in treating, e.g., cancer and inflammatory
PT diseases comprises at least one mutated CDR3 region.
PT
XX
PS Claim 22; SEQ ID NO 74; 80bp; English.
XX
XX The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined
CC sequence of 6 amino acids. A construct of the invention has
CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
CC immunosuppressive activity. The polypeptide construct, polynucleotide,
CC vector or composition are useful for the prevention, treatment or
CC amelioration of a proliferative disease, a tumorous disease, an
CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence encodes
CC bioprecise single chain antibody scFv EpcAMxCD3 with the M13 mutant
XX peptide in the anti CD3 region.
XX
SO Sequence 1479 BP; 387 A; 364 C; 388 G; 340 T; 0 U; 0 Other;

Query Match 67.2%; Score 480; DB 13; Length 1479;
Best Local Similarity 81.5%; Pred. No. 1.9e-129;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY 3 TATGTGATGACCCAGACTCCCAATTCCTGCTTGTATCAGCAGAGAGAGGGTTACAT 62
Db 3 TATCAGCTGACCCAGTCTCAAAAATTCATGTCCATCATAGTAGAGACAGGGTCAGGT 62
QY 63 AACCTGAAAGCCAGTACAGTGTGATTAATGATGTGGCTTGTACCAACAGAACCCAG 122
Db 63 CACCTGCAAGGCCAGTACAGATGTGGGTATCTAAATGTAGCCCTGTATCAACGAAACAG 122
QY 123 GCAGTCTCCGAACTGCTGATATACCTGTGATCCAAATGCTACACTGAGTCCCTGATCG 182
Db 123 GCAATCTCTTAAACACATGATTTACTCGGCACTCTACCGGTACAGTGGAGTCCCTGATCG 182
QY 183 CTTGACTGGCAGTGGATATGAGGACGATTTTCACTTACCATTCAGCACTGAGCGAGCTGA 242
Db 183 CTTGACAGGACGTGATCTGGGACAGATTTCACTCTCAACATCAGCAATGTGCACTGTGA 242
QY 243 AGACCTGAGATTATTTCTGTGACAGATTTATAGCT-----CGCTCGAGAGGGGG 293
Db 243 AGACTTGGCAGAGATTTCTGTGACAGATTTATACAGCTATCCGCTCAGCTGCTGCTGG 302
QY 294 GACCAAGCTGAAATTAAGGTGAGCGGTTCAAGCGGAGTGGCTTGGCGGTTGCGG 353
Db 303 GACCAAGCTGAGATCAAAAGGTGGTGGTCTGGCGCGCGGCTCCGGTGGTGGTGG 362
QY 354 ATGCGAGGTGACAGTGAAGAGATGACAGACCTGGCTGTGGTGGCGGCTTCAAGACCTGTG 413
Db 363 TTCTCAGGTGAACATGACAGAGATGACAGACCTGGCTGTGGTGGCGGCTTCAAGACCTGTG 422
QY 414 CATCACTTGCACCTGTCTGTGGTTTTCATTAAACCAATTATGTTGATCACTGGTTCGCCA 473
Db 423 CATCACTTGCACAGTCTCTGTGTTCTGTATTAACCTGATATGTTGATCACTGGTTCGCCA 482
QY 474 GCTTCAGAAAGGCTGTGAGTGGCTGGGAGTAAATGCGCTGTGGAGACAAATTA 533
Db 483 GTCTCAGAAAGGCTGTGAGTGGCTGGGAGTAAATGAGTGGTGGAGACAACTA 542
QY 534 TAATTCGGCTCTTATGTCCAGACTGACATTCAGAAAGACAACTCCAAAGCCAAAGTTT 593
Db 543 TAATGACGCTTTCATATCCAGACTGACATTCAGAAAGACAAATTCCAAGGCCAAAGTTT 602
QY 594 CTTAAAAATGAACTGTGCAAACTGATGACACAGCCATGACTACTGTGCGCAAGTGGG 653
Db 603 CTTAAAAATGAACTGTGCAAGCTAAATGACACAGCCATATATTACTGTGCGCAAGTGG- 661
QY 654 GGGTAACTACGCTATGCTTTGGAATCACTAGGGGTCAAGAACTCAGTCACCGTCTCTC 713
Db 662 -----AGAACTGTGCTTTGCTTACTGCGGCGCAAGGACCAAGTCACCGTCTCTC 713

RESULT 9
ADS99446
ID ADS99446 standard; DNA; 1479 BP.
XX
XX ADS99446;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Antibody scFv EpcAMxCD3 with M31 mutant in anti CD3 region encoding DNA.
DE
XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
KW immunological disorder; autoimmune disease; infectious disease;
KW scFv EpcAMxCD3; antibody; ds.
XX
OS Synthetic.
OS Unidentified.

XX
FH Key Location/Qualifiers
FT 1.1479
FT CDS /tag= a
FT /product= "scFv EpcAMxCD3 with M31 mutant in anti CD3
FT region"

QY 414 CATCACTTGACATGCTCTGCGGTTTTCATTAAACCAATTATGCTGACATGCGGTTCCCA 473
DB 423 CATCACTTGACATGCTCTGCGGTTTTCATTAACTAGTATGCTGACATGCGGTTCCCA 482
QY 474 GCTTCCAGGAAAGGCTTGGAGTGGCTGGGAGTATATGCGCTGGTGGAGCAAAATTA 533
DB 483 GTCTCCAGGAAAGGCTTGGAGTGGCTGGGAGTATATGCGCTGGTGGAGCAAAATTA 542
QY 534 TAAATGCGGCTCTTATGCTCAGACTGAGCATCAGCAAGCAACCTCCAAAGGCCAAGTTT 593
DB 543 TAAATGCGGCTCTTATGCTCAGACTGAGCATCAGCAAGCAACCTCCAAAGGCCAAGTTT 602
QY 594 CTTAAATAATGAACAGTCTGCAAACTGATGACAGAGCCATGACTACTGTCGAGTCGCGG 653
DB 603 CTTAAATAATGAACAGTCTGCAAACTGATGACAGAGCCATGACTACTGTCGAGTAATGG- 661
QY 654 GGGTAAGTACGCGCTATGCTTTGAGACTACTGCGGCTCAAGGAACCTCACTGCTCTCTC 713
DB 662 -----AGAACTGGTGGTTGCTTACTGCGGCGCAAGGACCAAGGTCAAGCTCTCTCTC 713

RESULT 12

ADSS99430
ID ADSS99430 standard; DNA; 1479 BP.

AC ADSS99430;

DT 02-DEC-2004 (first entry)

DE Antibody scFv EpcMxCD3 with M4 mutant in anti CD3 region encoding DNA.

KW CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;

KW immunosuppressive; proliferative disease; tumour; inflammatory disease;

KW immunological disorder; autoimmune disease; infectious disease;

KW scFv EpcMxCD3; antibody; ds.

OS Synthetic.

OS Unidentified.

XX

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XX

XX

XX

XX

XX

CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence encodes
CC bispecific single chain antibody scFv EpcMxCD3 with the M4 mutant
CC peptide in the anti CD3 region.
XX
SQ Sequence 1479 BP; 385 A; 364 C; 390 G; 340 T; 0 U; 0 Other;
Query Match 67.2%; Score 480; DB 13; Length 1479;
Best Local Similarity 81.5%; Pred. No. 1.9e-129;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

RESULT 13

ADSS99442
ID ADSS99442 standard; DNA; 1479 BP.

AC ADSS99442;

DT 02-DEC-2004 (first entry)

DE Antibody scFv EpcMxCD3 with M4 mutant in anti CD3 region encoding DNA.

KW CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;

KW immunosuppressive; proliferative disease; tumour; inflammatory disease;

KW immunological disorder; autoimmune disease; infectious disease;

KW scFv EpcMxCD3; antibody; ds.

OS Synthetic.

OS Unidentified.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

KM scFv EpcAMxCD3; antibody; ds.
 XX Synthetic.
 OS Unidentified.
 XX
 FH Key
 FT CDS
 FT
 FT Location/Qualifiers
 FT 1.1479
 FT /tag= a
 FT /product= "scFv EpcAMxCD3 with M14 mutant in anti CD3
 FT region"
 FT /note= "No start codon"
 FT
 PN CA2403313-A1.
 PD 11-APR-2004.
 XX
 XX 11-OCT-2002; 2002CA-02403313.
 PF
 XX 11-OCT-2002; 2002CA-02403313.
 PR
 XX 11-OCT-2002; 2002CA-02403313.
 XX
 PA (MICR-) MICROMET AG.
 XX
 XX Lanzavecchia A;
 PI
 XX
 DR WPI: 2004-390792/37.
 DR P-PSDB; ADS99441.
 XX
 XX
 PT Antibody construct, useful in treating, e.g., cancer and inflammatory
 PT diseases comprises at least one mutated CDR3 region.
 XX
 XX
 PS Claim 22; SEQ ID NO 76; 80bp; English.
 XX
 CC The invention relates to a novel polypeptide construct comprising at
 CC least one CDR3 region comprising at least one mutation in a fully defined
 CC sequence of 6 amino acids. A construct of the invention has
 CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
 CC immunosuppressive activity. The polypeptide construct, polynucleotide,
 CC vector or composition are useful for the prevention, treatment or
 CC amelioration of a proliferative disease, a tumorous disease, an
 CC inflammatory disease, an immunological disorder, an autoimmune disease or
 CC an infectious disease in a human subject. The present sequence encodes
 CC bispecific single chain antibody scFv EpcAMxCD3 with the M14 mutant
 CC peptide in the anti CD3 region.
 CC
 XX
 XX Sequence 1479 BP; 385 A; 364 C; 389 G; 341 T; 0 U; 0 Other;
 SQ
 Query Match 67.2%; Score 480; DB 13; Length 1479;
 Best Local Similarity 81.5%; Pred. No. 1.9e-129;
 Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
 QY 3 TATTGTGATGACCCAGACTCCCAATTCTGCTGTATACAGAGAGACAGGGTTACCAT 62
 DB 3 TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGAGACAGGGTCAAGCGT 62
 QY 63 AACCTGAGGCGCAGTCAAGTGTGAGTAATGATGTGCTGTGACCAAGAGAGCCAG 122
 DB 63 CACCTGAGGCGCAGTCAAGTGTGAGTAATGATGTGACCAAGAGAGCCAG 122
 QY 123 GCACTCTCCGAAATGCTGATATCTGATCCCAATGCTACACTGAGAGTCCCTGATCG 182
 DB 123 GCAATCTCTTAAACATGATTTACTCGGCATCTTACCGGTACAGTGAAGTCCCTGATCG 182
 QY 183 CTTTCACTGGCAGTGTGATATGAGACGATTTTCACTTTCACATCAGACACTGTGCAAGGCTGA 242
 DB 183 CTTTCACTGGCAGTGTGATATGAGACGATTTTCACTTTCACATCAGACACTGTGCAAGGCTGA 242
 QY 243 AGACTTGGCAATTTATTTCTGTGACGAGATTAATGCT-----CGCTCGAGAGGGG 293
 DB 243 AGACTTGGCAATTTATTTCTGTGACGAGATTAATGCT-----CGCTCGAGAGGGG 293
 QY 294 GACCAAGCTGGAATTAAGAGTGAAGCGGTTTCAGAGCGAGAGTGTGCGG 353
 DB 294 GACCAAGCTGGAATTAAGAGTGAAGCGGTTTCAGAGCGAGAGTGTGCGG 353
 QY 303 GACCAAGCTGGAATTAAGAGTGAAGCGGTTTCAGAGCGAGAGTGTGCGG 362
 DB 303 GACCAAGCTGGAATTAAGAGTGAAGCGGTTTCAGAGCGAGAGTGTGCGG 362

QY 354 ATGCAGATGACAGTGAAGAGTCAAGACCTGACCTGTGAGCCCTCACAAGAGCCTGTC 413
 DB 363 TTCTCAGATGAAGTCAAGAGTCAAGACCTGACCTGTGAGCCCTCACAAGAGCCTGTC 422
 QY 414 CATCACTTGAACCTGTCTCTGAGTTTTCATTAAACCAATTAATGTGTACACTGGGTTGCCCA 473
 DB 423 CATCACTTGAACCTGTCTCTGAGTTTTCATTAAACCAATTAATGTGTACACTGGGTTGCCCA 482
 QY 474 GCTTCCAGAAAGGTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 533
 DB 483 GCTTCCAGAAAGGTTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 542
 QY 534 TAATTCGCTCTTATGTCACAGACTGACATCAGCAAGCACTCAAGAGCCAGTTT 593
 DB 543 TAATTCGCTCTTATGTCACAGACTGACATCAGCAAGCACTCAAGAGCCAGTTT 602
 QY 594 CTTAAATATGAACAGTGTGCAAACTGATGACACAGCCATGTACTACTGTGCGAGTGGG 653
 DB 603 CTTTAAATATGAACAGTGTGCAAGCTGATGATGACACAGCCATGTACTACTGTGCGAGATGG- 661
 QY 654 GGGTAATCAAGGCTATGCTTGTGACTGTGGGGTCAAGAACTCACTCACTGCTCTC 713
 DB 662 -----AGAACTGTGTGCTTGTGACTGTGGGGTCAAGAACTCACTCACTGCTCTC 713
 RESULT 14
 ADS99432
 ID ADS99432 standard; DNA; 1479 BP.
 XX
 XX ADS99432;
 AC
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Antibody scFv EpcAMxCD3 with M7 mutant in anti CD3 region encoding DNA.
 XX
 CC CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
 CC immunosuppressive; proliferative disease; tumor; inflammatory disease;
 CC immunological disorder; autoimmune disease; infectious disease;
 CC scFv EpcAMxCD3; antibody; ds.
 KW
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 1.1479
 FT /tag= a
 FT /product= "scFv EpcAMxCD3 with M7 mutant in anti CD3
 FT region"
 FT /note= "No start codon"
 FT
 PN CA2403313-A1.
 PD 11-APR-2004.
 XX
 XX 11-OCT-2002; 2002CA-02403313.
 PF
 XX 11-OCT-2002; 2002CA-02403313.
 PR
 XX 11-OCT-2002; 2002CA-02403313.
 XX
 PA (MICR-) MICROMET AG.
 XX
 XX Lanzavecchia A;
 PI
 XX
 DR WPI: 2004-390792/37.
 DR P-PSDB; ADS99431.
 XX
 XX
 PT Antibody construct, useful in treating, e.g., cancer and inflammatory
 PT diseases comprises at least one mutated CDR3 region.
 XX
 XX
 PS Claim 22; SEQ ID NO 66; 80bp; English.
 XX
 CC The invention relates to a novel polypeptide construct comprising at
 CC least one CDR3 region comprising at least one mutation in a fully defined

Db 243 AGACTTGGCAGAGTATTTCTGTGACCAATATTAACAGTATCCGCTCAGGTTGGGTGCTG 302
QY 294 GACCAAGCTGGAATTAAGTGGAGCGGTTCAAGCCGAGTGCTCTGGCGGTGGCGG 353
Db 303 GACCAAGCTCAGATCAAAAGGTGGGTGCTTGGCGGCGGCGGCTCCGGTGGGTGG 362
QY 354 ATCCAGGTTGAGGTAAGAGTCAAGACTGGCCTGGGCGCCCTCACAAGGCTGTC 413
Db 363 TTCTCAGGTGAAGTGCAGAGTCAAGACTGGCCTTATGTCAGCCCTCACAAGGCTGTC 422
QY 414 CATCACTTGCACGTGCTCTGGGTTTTCATTAAACCAATTATGTTACACTGGGTTGCGCA 473
Db 423 CATCACTTGCACAGTCTGTTGTTCTCATTAAGTATGTTGACACTGGGTTGCGCA 482
QY 474 GCTTCCAGGAAAGGCTCTGAGTGGCTGGAGTAAATAGGGCTGTTGGAAGCACAATTA 533
Db 483 GTCTCCAGGAAAGGCTCTGAGTGGCTGGAGTAAATAGGGCTGTTGGAAGCACAAGCTA 542
QY 534 TAATTGGGCTCTTAATGTCAGACTGAGCATCAGCAAGGACAACCTCAAGGCAAGTTT 593
Db 543 TAATGCACTTTTCATATTCAGACTGAGCATCAGCAAGGACAATTCAGAGGCAAGTTT 602
QY 594 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAGTGGCCAGTGGGG 653
Db 603 CTTTAAATGAACAGTCTGCAAGCTATGACACAGCCATATATTACTGTGCCAAGATGG- 661
QY 654 GGGTAAGTACGGCTATGCTTGGACTACTGGGGTCAAGGAACCTCAGTCCCGTCTCTC 713
Db 662 -----AGAACTGGTGTGTTGCTTACTGGGGGCCAAGGACCAAGGTCCACCGTCTCTCTC 713

Search completed: February 18, 2005, 20:38:23
Job time : 422.122 secs

Db 241 GAAGACCTGGCAGTTTATTTCTGTGACAGAGATTATAGCTGCTCGAGAGGGGGACCAAG 300
Qy 301 CTGGAATAAAGGTGAGGCGGTTTCAGGGGAGGTGGCTCTGGCGGTGGCGATGCGAG 360
Db 301 CTGGAATAAAGGTGAGGCGGTTTCAGGGGAGGTGGCTCTGGCGGTGGCGATGCGAG 360
Qy 361 GTGCAAGTGAAGAGTCAAGACCTGGCTGGGCGGCTTCACAGAGCTGTCCATCACT 420
Db 361 GTGCAAGTGAAGAGTCAAGACCTGGCTGGGCGGCTTCACAGAGCTGTCCATCACT 420
Qy 421 TGCACGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTGGCAGCTTCA 480
Db 421 TGCACGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTGGCAGCTTCA 480
Qy 481 GGAAGGGCTGAGAGTGGAGTAAATAGGGCTGGTGGAAAGCAAAATTATTAATTCG 540
Db 481 GGAAGGGCTGAGAGTGGAGTAAATAGGGCTGGTGGAAAGCAAAATTATTAATTCG 540
Qy 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Db 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Qy 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAGTGTGCGAGTGGGGGGTAA 660
Db 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAGTGTGCGAGTGGGGGGTAA 660
Qy 661 TAGGGCTATGCTTTGAGCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714
Db 661 TAGGGCTATGCTTTGAGCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714

RESULT 2

US-09-142-974B-4
; Sequence 4, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Pen
; APPLICANT: Rivlin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain Fv Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK.P-013-USNP
; CURRENT APPLICATION NUMBER: US/09/142,974B
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/US97/04427
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,703
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: 3G6-scfv-streptavidin
US-09-142-974B-4

Query Match 100.0%; Score 714; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 1,5e-208;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGTGTATGACCCAGATCTCCCAAAATTCCTGTTGTATCAGCAGAGACAGGGTTACC 60
Db 1 AGTATGTGTATGACCCAGATCTCCCAAAATTCCTGTTGTATCAGCAGAGACAGGGTTACC 60
Qy 61 ATAACCTGAAGGCGAGTCAAGTGTAGTATGATGTGGCTGTGTAACCAAGAGGCCA 120
Db 61 ATAACCTGAAGGCGAGTCAAGTGTAGTATGATGTGGCTGTGTAACCAAGAGGCCA 120

Qy 121 GGGCAGTCTTCGAAACTGTGATATATCTGTACATCCATGCTACACTGGAGTCCCTGAT 180
Db 121 GGGCAGTCTTCGAAACTGTGATATATCTGTACATCCATGCTACACTGGAGTCCCTGAT 180
Qy 181 CGCTTCACTGGCAGTGTGATATGGGACGATTTTCACTTTCAACCATCAGCACTGTGAGGCT 240
Db 181 CGCTTCACTGGCAGTGTGATATGGGACGATTTTCACTTTCAACCATCAGCACTGTGAGGCT 240
Qy 241 GAAGACCTGGCAGTTTATTTCTGTGACAGAGATTATAGCTCGCTGGAGGGGGACCAAG 300
Db 241 GAAGACCTGGCAGTTTATTTCTGTGACAGAGATTATAGCTCGCTGGAGGGGGACCAAG 300
Qy 301 CTGGAATAAAGGTGAGGCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGATGCGAG 360
Db 301 CTGGAATAAAGGTGAGGCGGTTTCAGGCGAGGTGGCTCTGGCGGTGGCGATGCGAG 360
Qy 361 GTGCAAGTGAAGAGTCAAGACCTGGCTGGGCGGCTTCACAGAGCTGTCCATCACT 420
Db 361 GTGCAAGTGAAGAGTCAAGACCTGGCTGGGCGGCTTCACAGAGCTGTCCATCACT 420
Qy 421 TGCACGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTGGCAGCTTCA 480
Db 421 TGCACGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGGTTGGCAGCTTCA 480
Qy 481 GGAAGGGCTGAGAGTGGAGTAAATAGGGCTGGTGGAAAGCAAAATTATTAATTCG 540
Db 481 GGAAGGGCTGAGAGTGGAGTAAATAGGGCTGGTGGAAAGCAAAATTATTAATTCG 540
Qy 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Db 541 GCTCTTATGTCCAGACTGAGCATCAGCAAGCAACTCCAAAGCCAAAGTTTCTTAAAA 600
Qy 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAGTGTGCGAGTGGGGGGTAA 660
Db 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAGTGTGCGAGTGGGGGGTAA 660
Qy 661 TAGGGCTATGCTTTGAGCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714
Db 661 TAGGGCTATGCTTTGAGCTACTGGGGTCAAGAAACCTCAGTCAACCGTCTCTCA 714

RESULT 3

US-08-756-416-31
; Sequence 31, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Fell, Perry
; APPLICANT: Miltner, Robert
; APPLICANT: Winberg, Robert
; TITLE OF INVENTION: MODIFIED SPV MOLECULES WHICH
; TITLE OF INVENTION: MEDIANE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755

Db 241 GTGAGAGAGATGATATGCAATGATTTCTGTCAGCAAGTAGAAGGTTCTCTGACG 300
QY 283 CTGAGAGGGGGAGCAAGCTGGAATATAA--GGTGAAGCGGTTTCAGGCGGAGGTGC 339
Db 301 TTGGGTGAGAGGCAACAGCTGGAATCAACGGGGTGGCGGTGCTGGCGGGGTGGG 360
QY 340 TCTGGGGGTGGCGGATGCGAGGTGAGAGGAGTCAAGACCTGGCGGTGGGCGCC 399
Db 361 TCGGTTGGCGCGGATCTCAGGTGACGTAAAGAGTCAAGACCTGGCGGTGGGCGCC 420
QY 400 TCACAGAGCCTGTCATCACTTGACCTGCTCTGGGTTTCAATTAACCAATTATGTGA 459
Db 421 TCACAGAGCCTGTCATCACTTGACCTGCTCTGGGTTTCAATTAACCGGCTATGTGA 480
QY 460 CACTGGGTGGCGGACCTCCAGAGAGGGTCTGAGTGGCTGGAGTAATATGGCTGT 519
Db 481 AACTGGGTGGCGGACCTCCAGAGAGGGTCTGAGTGGCTGGAGTAATATGGGTGAT 540
QY 520 GGAAGCAAAATTAATATGGGCTTAATGTCAGACTGAGCATCAGCAAGGCAACTCC 579
Db 541 GGAAGCAAAATTAATATGAGCTCTCAAAATCCAGACTGAGCATCAGCAAGGCAACTCC 600
QY 580 AAGAGCCAACTTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 639
Db 601 AAGAGCCAACTTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 660
QY 640 TGTGCGAGTGGGGGGGTAACTAC-----GGCTATGCTTGAATATGAGGCTCAAGGA 693
Db 661 TGTGCGAGATGATGATTAATGTAATCTTCAATTAATGATGATGAGTACTGAGGCTCAAGGA 720
QY 694 ACCTCAGTCAACCGTCTCTC 713
Db 721 ACCTCAGTCAACCGTCTCTC 740

RESULT 5
US-08-756-416-29
; Sequence 29, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Mittleer, Robert
; APPLICANT: Winberg, Robert
; TITLE OF INVENTION: MODIFIED SPV MOLECULES WHICH
; TITLE OF INVENTION: MEDIANE ADHESION BETWEEN CELLS AND USES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: 'USA'
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/007,755
; FILING DATE: 30-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Aditano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436,41US01

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; TELNET:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1527 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-756-416-29

Query Match 58.0%; Score 414.4; DB 4; Length 1527;
Best Local Similarity 76.9%; Pred. No. 1.2e-116;
Matches 569; Conservative 0; Mismatches 141; Indels 30; Gaps 4;

QY 4 ATGTGATGACCCAGAGCTCCCAATTCCTGCTTGTATTCAGACAGAGAGGTTACATTA 63
Db 1 ATGTGCTCACCCCAATTCCTGCTTGTATTCAGAGAGGTTACATTA 60
QY 64 ACCTGCAAGCCAGTCAAGTGTGATTAATGATGGCT-----TGTACCA 111
Db 61 TCTGCAAGCCAGTCAAGTGTGATTAATGATGGCT-----TGTACCA 120
QY 112 CAGAACCCAGGCGAGTCTCCGAAATCTGCTGATTAATTCAGATCCCAATGCTACATGA 171
Db 121 CAGAAACAGAGAGGCGAGTCTCCGAAATCTGCTGATTAATTCAGATCCCAATGCTAC 180
QY 172 GTCCCTGATGCTTCACTGCGAGTGTATGAGACGGAATTCACCTTTCACATCACTG 231
Db 181 GTCCCTGATGCTTCACTGCGAGTGTATGAGACGGAATTCACCTTTCACATCACTG 240
QY 232 GTGCAAGCTGAAAGCTGCGAGTTATTTCTGTACG-----AGATTAATGACTG 282
Db 241 GTGAGAGAGATGATTAATGCAATGTAATTTCTGTCAAGCAAGAGGTTCTTGAAG 300
QY 283 CTGAGAGGGGGAGCAAGCTGGAATAAATAA-----GGTGAAGGGGTTCAAGCGGAGGTGC 339
Db 301 TTGGGTGAGAGGCAACAGCTGGAATAAATAAAGGGGTTGAGGCTGGGCGGTGGG 360
QY 340 TGTGCGGTGGGGGATGCGAGGTGAGAGGAGTCAAGACCTGCTGCTGGGCGCC 399
Db 361 TGTGCGGTGGGGGATGCGAGGTGAGAGGAGTCAAGACCTGCTGCTGGGCGCC 420
QY 400 TCACAGAGCCTGTCATCACTTGACCTGCTCTGGGTTTCAATTAACCAATTATGTGTA 459
Db 421 TCACAGAGCCTGTCATCACTTGACCTGCTCTGGGTTTCAATTAACCGCTATGTGTA 480
QY 460 CACTGGGTGGCGAGCTCCAGAGAGGGTCTGAGTGGCTGGAGTAATATGGGCTGAT 519
Db 481 AACTGGGTGGCGAGCTCCAGAGAGGGTCTGAGTGGCTGGAGTAATATGGGCTGAT 540
QY 520 GGAAGCAAAATTAATATGGGCTTAATGTCAGACTGAGCATCAGCAAGGCAACTCC 579
Db 541 GGAAGCAAAATTAATATGGGCTTAATGTCAGACTGAGCATCAGCAAGGCAACTCC 600
QY 580 AAGAGCCAACTTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 639
Db 601 AAGAGCCAACTTTCTTAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTAC 660
QY 640 TGTGCGAGTGGGGGGGTAACTAC-----GGCTATGCTTGAATATGAGGCTCAAGGA 693
Db 661 TGTGCGAGATGATGATTAATGTAATCTTCAATTAATGATGATGAGTACTGAGGCTCAAGGA 720
QY 694 ACCTCAGTCAACCGTCTCTC 713
Db 721 ACCTCAGTCAACCGTCTCTC 740

RESULT 6
5455030-16
; Patent No. 5455030

```

; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 16:
; LENGTH: 729
5455030-16

Query Match      57.2%; Score 408.2; DB 6; Length 729;
Best Local Similarity 75.8%; Pred. No. 6.9e-115;
Matches 548; Conservative 0; Mismatches 163; Indels 12; Gaps 3;

Oy 4 ATTGATGACCCAGACTCCCAATTCTGCTGTATGACAGAGAGAGAGGTTACATA 63
Db 7 AATGCTCACCCAGCTCCAGCATATGCTGATCTCCAGGGGAAAAGTCACCATG 66
Oy 64 ACCTGCAAGGCGAGTCAGAGTGTAGT---AATGATGCGCTGGTACCAAGAACCA 120
Db 67 ACCTGCAAGGCGAGTCAGAGTGTAGT---AATGATGCGCTGGTACCAAGAACCA 126
Oy 121 GGGCAGTCTCCGAAACTGCTGATATCTCTGATCTCAATCGCTACCTGAGTCCGTAT 180
Db 127 GGTCCCTCCCAAACTCTGGGTTTATGCGACATCCAACTTGGCTCTGGAGTCCCTG 186
Oy 181 CGCTTCATGCGAGTGATATGGGACGGAATTTCACTTTCACCATCAGACATGCGAGCT 240
Db 187 CGCTTCATGCGAGTGATATGGGACGGAATTTCACTTTCACCATCAGACATGCGAGCT 246
Oy 241 GAAGACCTGGCAGTTTATTTCTGTACAGCAG-----GATTATAGCTCGCTCGAGGGGG 294
Db 247 GAAGATGCTGCACCTTATTTACTGTCTAGCAGTACAGTGTATAGGACTACGTTGGTCT 306
Oy 295 ACCAAGCTGGAATTAAGAGTGTGAGGCGGTTCAAGCGAGGTGCTCTGGCGTGGCGGA 354
Db 307 CCCACCAAGCTTAAGAGTGTGAGTGTGAGGCGGTTCAAGCGAGGTGCTCTGGCGTGGCGGA 366
Oy 355 TCGCAGGTGCGAGTGAAGAGTCAAGGACCTGGGCGGCGCTCCACAGAGCTGTCC 414
Db 367 CTGAGTGTGCGAGTGAAGAGTCAAGGACCTGGGCGGCGCTCCACAGAGCTGTCC 426
Oy 415 ATCATCTGCACTGTCTCTGGGTTTTTCATTAAACAATTATGTTGATCACTGGGTTGCGCAG 474
Db 427 ATCATCTGCACTGTCTCTGGGTTTTTCATTAAACAATTATGTTGATCACTGGGTTGCGCAG 486
Oy 475 CCTCAGAGAAAGGCTCTGAGTGTGCGAGTGAATATATGAGTGTGAGGACAATAATAT 534
Db 487 CCTCAGAGAAAGGCTCTGAGTGTGCGAGTGAATATATGAGTGTGAGGACAATAATAT 546
Oy 535 AATTGCGCTCTTATGTCCAGACTGAGATCAAGCAAGGACCACTCCAAAGGCAAGTTTC 594
Db 547 AATTGCGCTCTTATGTCCAGACTGAGATCAAGCAAGGACCACTCCAAAGGCAAGTTTC 606
Oy 595 TTAATAATGACAGCTCTGCAAGTATGATGACACAGGCTACTACTGTGCA---GTGCG 651
Db 607 TTAATAATGACAGCTCTGCAAGTATGATGACACAGGCTACTACTGTGCA---GTGCG 666
Oy 652 GGGGGTAACTACGGGTATGCTTTGAGTACTAGGGGTCAAGGAAGCTCAGTACCGGTCTCC 711
Db 667 GAACGAATCTTTTACTATGATGATGAGTATGGGGTCAAGGAAGCTCAGTACCGGTCTCC 726
Oy 712 TCA 714
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Db 727 TAA 729

RESULT 7
5455030-16
Patent No. 5455030
APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
POLYPEPTIDE BINDING MOLECULES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
SEQ ID NO: 16:
LENGTH: 729
5455030-16

Query Match      57.2%; Score 408.2; DB 6; Length 729;
Best Local Similarity 75.8%; Pred. No. 6.9e-115;
Matches 548; Conservative 0; Mismatches 163; Indels 12; Gaps 3;

Oy 4 ATTGATGACCCAGACTCCCAATTCTGCTGTATGACAGAGAGAGGTTACATA 63
Db 7 AATGCTCACCCAGCTCCAGCATATGCTGATCTCCAGGGGAAAAGTCACCATG 66
Oy 64 ACCTGCAAGGCGAGTCAGAGTGTAGT---AATGATGCGCTGGTACCAAGAACCA 120
Db 67 ACCTGCAAGGCGAGTCAGAGTGTAGT---AATGATGCGCTGGTACCAAGAACCA 126
Oy 121 GGGCAGTCTCCGAAACTGCTGATATCTCTGATCTCAATCGCTACCTGAGTCCGTAT 180
Db 127 GGTCCCTCCCAAACTCTGGGTTTATGCGACATCCAACTTGGCTCTGGAGTCCCTG 186
Oy 181 CGCTTCATGCGAGTGATATGGGACGGAATTTCACTTTCACCATCAGACATGCGAGCT 240
Db 187 CGCTTCATGCGAGTGATATGGGACGGAATTTCACTTTCACCATCAGACATGCGAGCT 246
Oy 241 GAAGACCTGGCAGTTTATTTCTGTACAGCAG-----GATTATAGCTCGCTCGAGGGGG 294
Db 247 GAAGATGCTGCACCTTATTTACTGTCTAGCAGTACAGTGTATAGGACTACGTTGGTCT 306
Oy 295 ACCAAGCTGGAATTAAGAGTGTGAGGCGGTTCAAGCGAGGTGCTCTGGCGTGGCGGA 354
Db 307 CCCACCAAGCTTAAGAGTGTGAGTGTGAGGCGGTTCAAGCGAGGTGCTCTGGCGTGGCGGA 366
Oy 355 TCGCAGGTGCGAGTGAAGAGTCAAGGACCTGGGCGGCGCTCCACAGAGCTGTCC 414
Db 367 CTGAGTGTGCGAGTGAAGAGTCAAGGACCTGGGCGGCGCTCCACAGAGCTGTCC 426
Oy 415 ATCATCTGCACTGTCTCTGGGTTTTTCATTAAACAATTATGTTGATCACTGGGTTGCGCAG 474
Db 427 ATCATCTGCACTGTCTCTGGGTTTTTCATTAAACAATTATGTTGATCACTGGGTTGCGCAG 486
Oy 475 CCTCAGAGAAAGGCTCTGAGTGTGCGAGTGAATATATGAGTGTGAGGACAATAATAT 534
Db 487 CCTCAGAGAAAGGCTCTGAGTGTGCGAGTGAATATATGAGTGTGAGGACAATAATAT 546
Oy 535 AATTGCGCTCTTATGTCCAGACTGAGATCAAGCAAGGACCACTCCAAAGGCAAGTTTC 594
Db 547 AATTGCGCTCTTATGTCCAGACTGAGATCAAGCAAGGACCACTCCAAAGGCAAGTTTC 606
Oy 595 TTAATAATGACAGCTCTGCAAGTATGATGACACAGGCTACTACTGTGCA---GTGCG 651
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FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "cDNA domains with synthetic
IMMEDIATE SOURCE:
CLONE: EcoRI-HindIII insert of pUR4124
FEATURE:
NAME/KEY: CDS
LOCATION: 11..730
OTHER INFORMATION: /product= "VL1ys-GS-VH1ys"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 11..334
OTHER INFORMATION: /product= "VL1ys"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 335..379
OTHER INFORMATION: /product= "(Gly4Ser)3 linker"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 380..727
OTHER INFORMATION: /product= "VH1ys"
US-08-860-174A-1

Query Match 55.8%; Score 398.2; DB 2; Length 737;
Best Local Similarity 75.2%; Pred. No. 8e-112;

Matches 544; Conservative 0; Mismatches 158; Indels 21; Gaps 3;

4 ATTGTGATGACCCAGACATCCCAATTCCTGCTGTGATGAGCAGAGAGAGAGATTACATA 63
14 ATGAGCTCACCCAGTCTCCAGCTCCCTTCTGCTGAGGAGAAAGTGTACATC 73
64 ACCGCAAGCCAGTCAAGTGTGATGATGCTGCTGATACCAAGAGCAGGG 123
74 ACATGTCAGCAGAGGAGATATTCACATTAATTAGATGATACAGCAAGAGGA 133
124 CAGTCTCCGAAAGCTGATTAATCTGATCTGATCCATCGTACAGTGGAGTCCGTATGC 183
134 AATCTCTCAGCTCTGCTGCTATTAATCAACACCTTAGCAGATGCTGTCATCAAG 193
184 TTCACTGAGCATGATATGAGCAGGATTCATTACCATCAGACATGTCAGGCTGAA 243
194 TTCAGTGGCACTGATGATGAGAACACAAATATCTCTCAGATCAACAGCTCCAACTGAA 253
244 GACCTGCGAGTTTATTTCTGTACAGGATT-----ATAGCTGCTCGAGGGGGG 294
254 GATTTTGGAGTTATTAATCTGATCAATTTTGAAGTACTCTCGGACGTTGCGAGGG 313
295 ACCAAGCTGGAATTA---GTTGAGGCGGTTCAAGCGAGAGGCTGCTGGGCGTGGC 351
314 ACCAAGCTGAGATTAACGAGGAGGAGGCGTTTCAAGCGAGGAGGCTGCGGCGTGGC 373
352 GGATCGCAGTGCAGTGAAGAGTCAAGACCTGCTGCTGCGCCCTCAAGAGCTTG 411
374 GGATCGCAGTGCAGTGCAGTGAAGAGTCAAGACCTGCTGCTGCGCCCTCAAGAGCTTG 433
412 TCATCACTTGCATGCTGCTGCTGCTTTCATTAACCAATTAAGTGTAACCTGGGTTGC 471
434 TCATCACTTGCATGCTGCTGCTGCTTTCATTAACCAATTAAGTGTAACCTGGGTTGC 493
472 CAGCTCCAGGAAGGCTGAGTGGCTGGAGGATTAATAGGCTGAGGAGCAAAAT 531
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494 CAGCTCCAGGAAGGCTGAGTGGCTGGAAATGATTTGGGTGATGAAACAGAC 553
532 TATATTCGCTCTTAATGTCAGACTGAGCATGAGCAAGCACTCCAGAGCAAGTT 591
554 TATATTCAGCTCTCAATCCAGACTGAGCATGAGCAAGCAAGCACTCCAGAGCAAGTT 613
592 TTCTTAATAATGACAGTCTGCAACTGATGACAGCAGCATGTACTACTGTGCGAGTCGG 651
614 TTCTTAATAATGACAGTCTGCAACTGATGACAGCAGCATGTACTACTGTGCGAGAG 673
652 GGGGTAACCTAGCTGCTTGGACTGAGTGGGCTGAGAACTGAGTACCGCTCC 711
674 AGAAT-----TATAGCTTGAATGAGGCGCAAGGACACAGGTACCGCTCC 724
712 TCA 714
725 TCA 727

RESULT 10

US-09-171-025-23
Sequence 23, Application US/09171025
Patent No. 6239259
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Multivalent and multispecific antigen-binding

TITLE OF INVENTION: Protein

NUMBER OF SEQUENCES: 27

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/171,025

FILING DATE:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 737 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "cDNA domains with synthetic linker(s)"

IMMEDIATE SOURCE:

CLONE: EcoRI-HindIII insert of pUR4124

FEATURE:

NAME/KEY: CDS

LOCATION: 11..730

OTHER INFORMATION: /product= "VL1ys-GS-VH1ys"

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 11..334

OTHER INFORMATION: /product= "VL1ys"

FEATURE:

NAME/KEY: misc_RNA

LOCATION: 335..379

OTHER INFORMATION: /product= "(Gly4Ser)3 linker"

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 380..727

OTHER INFORMATION: /product= "VH1ys"

US-09-171-025-23

Query Match 55.8%; Score 398.2; DB 3; Length 737;
Best Local Similarity 75.2%; Pred. No. 8e-112;

Matches 544; Conservative 0; Mismatches 158; Indels 21; Gaps 3;

4 ATTGTGATGACCCAGACATCCCAATTCCTGCTGTGATGAGCAGAGAGAGATTACATA 63
14 ATGAGCTCACCCAGTCTCCAGCTCCCTTCTGCTGAGGAGAAAGTGTACATC 73
64 ACCGCAAGCCAGTCAAGTGTGATGATGCTGCTGATACCAAGAGCAGGG 123

Db 74 ACATGTCGACGAGTGGGAATATTCACAAATTAATTGACATGATCATGACAGAAACAGGGA 133
Qy 124 CAGTCTCCGAAACGCTGATATATCTCTGCATCCAAATGGCTACACTGAGTCCCTGATCCG 133
Db 134 AAATCTCTCAGCTCCCTGCTCTATTAACAACAACCTTACAGATGGTGTGCCATCAAG 133
Qy 184 TTCATGCGACGTGATATGAGACGATTTCACTTCCATCAGACTGTCAGAGCTGAA 243
Db 194 TTCATGCGACGTGATATGAGACCAATATTTCTCAGATTCACACCTGTCGACCTGAA 253
Qy 244 GACCTGCGACGTTATTTCTGTCTCAGCAGATT-----ATAGCTCGCTCGAGGCGGG 294
Db 254 GATTTGGAGATATTAATGTCACAACTTTTGGAGTACTCTCGAGCTTCGGGTGAGGG 313
Qy 295 ACCAAGCTGGAATAA---GGTGAAGGGGTTCCAGGCGGAGTGGCTCTGGCGGTGC 351
Db 314 ACCAAGCTGGAATAAAGGGGGTGAAGGGCGGTTCAAGCGAGGTGGCTCTGGCGGTGC 373
Qy 352 GGATCGCAGGTGCGAGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAGACAGGCTG 411
Db 374 GGATCGCAGGTGCGAGTGAAGAGTCAAGACCTGGCTGGTGGCGCCCTCAGACAGGCTG 433
Qy 412 TCCATCACTGCACTGTCTCTGGGTTTCAATTAACAATTAATGTTGATCACTGGGTTGC 471
Db 434 TCCATCACTGCACTGTCTCTGGGTTTCAATTAACAATGATGTTAACTGGGTTGC 493
Qy 472 CAGCTCCAGAAAGGCTGTGAGTGGCTGGAGATATATGGGCTGTGAGACACAAT 531
Db 494 CAGCTCCAGAAAGGCTGTGAGTGGCTGGAGATATATGGGCTGTGAGAAACACAGAC 553
Qy 532 TATAATTCGCTCTTATGTCAGACTGAGATCAGACGAACTCAAGAGCCAGTT 591
Db 554 TATAATTCGCTCTTATGTCAGACTGAGATCAGACGAACTCAAGAGCCAGTT 613
Qy 592 TTCTTAAATGAACAGCTGTGCAAACTGATGACACAGCCATGTACTACTGTCCAGTCCG 651
Db 614 TTCTTAAATGAACAGCTGTGCAAACTGATGACACAGCCATGTACTACTGTCCAGTCCG 673
Qy 652 GGGGTGATCAAGGCTATGCTTGGACTACTGGGGTCAAGAACTCAAGTCACTGTCC 711
Db 674 AGAAT-----TATAGCTTGACTACTGGGGCCAAAGGACACAGGTCACTGTCC 724
Qy 712 TCA 714
Db 725 TCA 727

RESULT 11
US-08-197-834-6
Sequence 6, Application US/08197834
Patent No. 5639455
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08197,834

FILED DATE: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 028173/1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblion, No. 5639455man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-661-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: DNA (synthetic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
US-08-197-834-6

Query Match 55.5%; Score 396.2; DB 1; Length 738;
Best Local Similarity 75.5%; Pred. No. 3.3e-111;
Matches 555; Conservative 0; Mismatches 153; Indels 27; Gaps 4;

Qy 4 ATTGATGATACCCAGATCCCAATTCCTGTTGATACAGAGAGAGAGGTTACCAT 63
Db 7 ATCTCTGACACAGCTCCAAATTCCTGTTGATACAGAGAGAGGTTACCAT 66
Qy 64 ACTGCAAGCCAGTGAAGTGTGATATGATGTGCTTGGTATCCAAAGAACAGG 123
Db 67 ACTGCAAGCCAGTGAAGTGTGATATGATGTGCTTGGTATCCAAAGAACAGG 126
Qy 124 CAGTCCGAACTGTGATATGATCTGATCCATTCGCTCACTGAGTCCCTGATCCG 183
Db 127 CAGTCTCTTAATCTGATATGATCTGATCCATTCGCTCACTGAGTCCCTGATCCG 186
Qy 184 TTCATGCGAGTGTGATATGAGACGATTTCACTTCAACATCAGACTGTGACGTGA 243
Db 187 TTCATGCGAGTGTGATATGAGACGATTTCACTTCAACATCAGACTGTGACGTGA 246
Qy 244 GACCTGCGAGTTATTTCTGTGACGAGATTATG-----CTGCTCGAGGGGG 294
Db 247 GACCTGCGAGTTATTTCTGTGACGAGATTATGAGTCTCACTTCACTGCTGGGG 306
Qy 295 ACCAAGCTGGAATAAAGGTGAGGCGGTTCAAGCGGAGGTGCTCTGGCGGTGCGGA 354
Db 307 ACCAAGCTGGAATAAAGGTGAGGCGGTTCAAGCGGAGGTGCTCTGGCGGTGCGGA 363
Qy 355 TCGCAGGTGAGTGAAGAGTCAAGACCTGGCTGGGCGCTCAAGAGCTGTCC 414
Db 364 AGCAGGTGAAATCGAGAGTCTGGCCCTGGGATTTGACGCCCTCCAGACCTCAAT 423
Qy 415 ATCACTGCACTGTCTGTGGGTTTCATTAACTTAAT-----GTTGATCACTGGTT 468
Db 424 CTGACTTGTCTTCTCTGGGTTTCTACAGAGACTTCTGATATGAGTGTGAGCTGAT 483
Qy 469 CGCAGCTTCAGAAAGGCTCTGAGTGGCTGGAGTAAATAGGCTGTGAGACACA 528
Db 484 CGTCAGCTTCAGAAAGGCTCTGAGTGGCTGGAGTAAATAGGCTGTGAGACACA 543
Qy 529 AATTATAATTCGCTCTTATGTCAGACTGAGATCAGACAGCAACTCAAGAGCCAA 588
Db 544 CACTATAACCATTCCTGAGAGCGGCTCACAATCTCCAGAGATACCTCAACAACAG 603
Qy 589 GTTTCTTAAATGAACAGTCTGCAACTGATGACACAGCCATGTACTGTGCTGAGT 648
Db 604 GTATTCCTCAAGATCAAGTGTGACACTGAGATATGCGACATATCTTGTGCTCGA 663

QY 649 CG-----GGGGGTAAGTACGAGCTTGTGACTACTAGGGGTCAAGAACTCTCA 699
DB 664 AGAAGTCTATATGTAATTTGGGGGACTATGACTATGACTACTAGGGGTCAAGAACTCTCA 723
QY 700 GTCAACGCTCTCTCTCA 714
DB 724 GTCAACGCTCTCTCTCA 738

RESULT 12

US-09-742-693-29
; Sequence 29: Application US/09742693
; Patent No. 6579842
; GENERAL INFORMATION:
; APPLICANT: HOWELL, Steven
; APPLICANT: LITTLE, Julie C.
; APPLICANT: VAN DER LOGT, Cornelis P.
; APPLICANT: BARRY, Neil J.
; TITLE OF INVENTION: METHOD OF TREATING FABRICS
; FILE REFERENCE: C7536 (V)
; CURRENT APPLICATION NUMBER: US/09/742,693
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: EP9310431.4
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-742-693-29

Query Match 1 55.3%; Score 394.8; DB 4; Length 734;

Best Local Similarity 75.0%; Pred. No. 8.8e-111;

Matches 540; Conservative 0; Mismatches 162; Indels 18; Gaps 3;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATGACGAGAGAGAGAGGTTACATA 63
DB 14 ATGAGGTGACCCAGCTCCAGCCCTCTCTGCTGTGAGGAAACGTCAACATC 73
QY 64 ACCTGCAAGGCAAGTCAAGTGTGATATGATGCTTGTGATCAACAGAGGCAAGG 123
DB 74 ACAGTGTGAGCAAGTGTGATATTCACAAATTTAGATGATATCAAGCAAGAGG 133
QY 124 CAGCTCCGAAACGCTGATATATCTGATCCAAATGCTACAGTGGAGTCCCTGATGC 183
DB 134 AAATCTCTCAGCTCTGCTGTATATTAACAACAACCTTACGAGATGCTGCTCAAG 193
QY 184 TTCACTGAGTATATGAGACGAGATTCCTTTCACATCAGACAGTGTGAGGCTGAA 243
DB 194 TTGAGTGTGAGTATGAGCAACAATATCTCTCAAGATCAACAGCTGTCAACCTGAA 253
QY 244 GACCTGCAAGTTATTTCTGTGAGAGGATTAATAGCTGCTGG-----AGGGGGAAC 297
DB 254 GATTGTGAGTATTTACTGTCAACATTTTGGAGTACTCTCCGACCTTGGGTGAAAC 313
QY 298 AAGCTGGAATAA-----GTTGAGAGGCTTCAAGCGAGGAGTGTGAGGCTGAGGGA 354
DB 314 AAGCTCGAGATCAACCGGAGGAGGAGGCTTCAAGCGAGGAGTGTGAGGCTGAGGGA 373
QY 355 TCGCAGGTGAGTGAAGAGTCAAGACCTGAGCTGTGAGGCTTCAAGAGCTGTCC 414
DB 374 TCGCAGGTGAGTGAAGAGTCAAGACCTGAGCTGTGAGGCTTCAAGAGCTGTCC 433
QY 415 ATCACTTGTGATGTCTGTGGTTTCAATTAACAATTAATGTGTACACTGGGTTGCGAG 474
DB 434 ATCACTGTGACCGTCTCAAGGTTTCAATTAACCGGCTATGTGTAAATGTGGTTGCGAG 493
QY 475 CCTCAGAGAAAGGCTGTGAGTGTGAGGATTAATATGAGGCTGGTGAAGCAAAATTA 534

DB 494 CCTCAGAGAAAGGCTGTGAGTGTGAGGATTAATTTGGGGTATGAAACAGACATAT 553
QY 535 AATTCGGCTCTTATGTCCAGCTGAGCATCAAGCAAGCAACTCAAGAGCAAGTTTC 594
DB 554 AATTCAGCTCTCAATCAAGCTGAGCATCAAGCAAGCAACTCAAGAGCAAGTTTC 613
QY 595 TTAATAATGAACAGTGTCAAACTGATGACACAGCCATGTACTAGTGTGAGGAGG 654
DB 614 TTAATAATGAACAGTGTGACACTGATGACACAGCCAGTACTAGTGTGAGGAGG 673
QY 655 GTTAAGTACGAGTATGCTTGTGACTACTGAGGCTCAAGAACTTCAAGTCAAGTCTCTCA 714
DB 674 GAT-----TATAGCTTGACTACTGAGGAGCAAGAGCAACGCTCACGCTCTCTCA 724

RESULT 13

5455030-14
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:14
; LENGTH: 720
5455030-14

Query Match 1 55.1%; Score 393.6; DB 6; Length 720;

Best Local Similarity 75.8%; Pred. No. 2e-110;

Matches 550; Conservative 0; Mismatches 149; Indels 27; Gaps 4;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATGACGAGAGAGAGGTTACATA 63
DB 7 AATGTGCTCACCCAGTCTCAAGCATATGATGTGATCTCCAGGAAAGTCAACATG 66
QY 64 ACCTGCAAGGCAAGTCAAGTGTGAT-----AATGATGTGCTTGTGATCAACAGAGCA 120
DB 67 ACCTGCAAGGCAAGTCAAGTGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 126
QY 121 GAGCAGTCTCCGAAACGCTGATATATCTGATCCAAATGCTACACTGAGATCCCTGAT 180
DB 127 GGTGCTCTCCCAAACTCTGGGTTATGAGCAATCCAACTGCTGTGAGTCCCTGCT 186
QY 181 CGCTTCACTGAGTGTATGAGAGGATTTTCACTTTCACATCAGACAGTGTGAGGCT 240
DB 187 CGCTTCACTGAGTGTGAGTGTGAGGATCTTCACTTTCACATCAGACAGTGTGAGGCT 246
QY 241 GAAGACCTGCAAGTTATTTCTGTGACAGAGATTAATG-----CTGCTGAGAGG 291
DB 247 GAAGATCTGCAACTTATTTCTGTGACAGAGTATGAGTGTGATCCATCAGATCTGCT 306
QY 292 GAGCAAGCTTGAATAAAGTGAAGGCGGTTCAAGCGAGAGTGTGAGGCTGTGCGG 351
DB 307 GAGCAAGCTTGAAGTGAAGGCTGAAGGTTAA-----TCTTCTGCTGTGCTTCCGAA 354
QY 352 GATTCGAGAGTGAAGTGAAGGAGTCAAGACCTGATGTGAGGCTTCAAGAGCTGTG 411
DB 355 TTTAATCTTCACTGAGTGAAGGAGTCAAGACCTGATGTGAGGCTTCAAGAGCTGTG 414
QY 412 TCCATCACTTGTGACTGTCTGTGGTTTCAATTAACAATTAATGTGTACACTGGGTTGCG 471
DB 415 TCCATCACTTGTGACTGTCTGTGGTTTCAATTAACAATTAATGTGTACACTGGGTTGCG 474

QY 472 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTATATGGCTGGTGAAGCAAAAT 531
| | | | |
Db 475 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTATATGGCTGGTGAAGCAAAAT 534
QY 532 TATTAATTCAGCTCTTATGTCGAGCTGAGCATGACAGAGACAATCCAAAGCCAAATT 591
| | | | |
Db 535 TATTAATTCAGCTCTTATGTCGAGCTGAGCATGACAGAGACAATCCAAAGCCAAATT 594
QY 592 TTCTTAAATTAAGACAGTCTGACAACTGATGACACAGCCATGATCTAGTGGCA---GT 648
| | | | |
Db 595 TTCTTAAATTAAGACAGTCTGACAAATGATGACACAGCCATGATCTAGTGGCAAAAGA 654
QY 649 CGGGGGGGTAACTACGAGCTATGCTTTGAGTAACTGGGGTCAAGAACTGACCGCTC 708
| | | | |
Db 655 CTGGAACGAATGTTTACTATGCTATGAGACTATTGGGGTCAAGGAACCTGACGCTGC 714
QY 709 TCCTCA 714
| | | | |
Db 715 TCCTAA 720

RESULT 14
5455030-14
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:14:
; LENGTH: 720
5455030-14

Query Match 55.1%; Score 393.6; DB 6; Length 720;
Best Local Similarity 75.8%; Pred. No. 2e-110; Indels 27; Gaps 4;
Matches 550; Conservative 0; Mismatches 149;

QY 4 ATTGTGATGACCCAGACTCCCAAAATTCCTGCTGTATCAGACAGAGACAGGGTTACCAT 63
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QY 64 ACCGCAAGCCAGCTCAGAGTGAAGT---AATGATGTGCTTGTGTCACAGAAAGCA 120
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Db 67 ACCGCAAGCCAGCTCAGAGTGAAGTTCAGATTACTTCCACTCTCCAGCAGAAAGTCA 126
QY 121 GGGGAGTCTCCGAAGCTGATATATCTGCAATCCAAATGCTTACATGAGTCCCGAT 180
| | | | |
Db 127 GGGGAGTCTCCGAAGCTGATATATCTGCAATCCAAATGCTTACATGAGTCCCGAT 186
QY 181 CGCTTCACTGGAGTGAATGAGACGGAATTTTCACATTTCACATCAGACATGTCAGAGCT 240
| | | | |
Db 187 CGCTTCACTGGAGTGAATGAGACGGAATTTTCACATTTCACATCAGACATGTCAGAGCT 246
QY 241 GAAGACCTGCAAGTTATTTCTGTGACAGAGATTAAAG-----CTGCTGGAGGG 291
| | | | |
Db 247 GAAGACCTGCAAGTTATTTCTGTGACAGAGATTAAAG-----CTGCTGGAGGG 306
QY 292 GGGACCAAGCTGGAATAAAGAGTGAAGGCGGTTCAAGGCGAGTGGCTTGGCGGGTGC 351
| | | | |
Db 307 GGGACCAAGCTGGAAGTGAAGGTTAA-----TCTTCTGGTTCTGGTTCCGAA 354

QY 352 GGATTCGACAGTGCAGGTGAAGAGTCAAGACCTGCGCTGGTGGCCGCTCAAGAGCCTG 411
| | | | |
Db 355 TCTAATTCATCAGCTGGAAGAGTCAAGACCTGCGCTGGTGGCCGCTCAAGAGCCTG 414
QY 412 TCCATACATTTGACATGCTCTGAGTTTTCATTAAACCAATTATGTTGTACATGCGGTTCCG 471
| | | | |
Db 415 TCCATACATTTGACATGCTCTGAGTTTTCATTAAACCAATTATGTTGTACATGCGGTTCCG 474
QY 472 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTAAATGAGGCTGGTGAAGCAAAAT 531
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Db 475 CAGCTTCAGAGAAAGGCTGAGTGGCTGGAGTAAATGAGGCTGGTGAAGCAAAAT 534
QY 532 TATTAATTCAGCTCTTATGTCGAGCTGAGCATGACAGAGACAATCCAAAGCCAAATT 591
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QY 592 TTCTTAAATTAAGACAGTCTGACAACTGATGACACAGCCATGATCTAGTGGCA---GT 648
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Db 655 CTGGAACGAATGTTTACTATGCTATGAGACTATTGGGGTCAAGGAACCTGACGCTGC 714
QY 709 TCCTCA 714
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Db 715 TCCTAA 720

RESULT 15
US-09-554-765-12
; Sequence 12, Application US/09554765
; Patent No. 6551495
; GENERAL INFORMATION:
; APPLICANT: Porter, Robert A
; APPLICANT: Badley, Robert A
; TITLE OF INVENTION: Electroactive Surfaces
; FILE REFERENCE: IMIN.P-036
; CURRENT APPLICATION NUMBER: US/09/554,765
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03495
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 739
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: bispecific scFv4155-HCV3 and HCV24 construct
US-09-554-765-12

Query Match 55.1%; Score 393.2; DB 4; Length 739;
Best Local Similarity 74.9%; Pred. No. 2.7e-110; Indels 18; Gaps 3;
Matches 539; Conservative 0; Mismatches 163;

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Db 134 AATATCTCCAGTCTCTGCTGTTATTAACAACCTTGAAGATGTTGTCATCAAG 193
QY 184 TTCACTGGAGTGAATGAGACGGAATTTTCACATTTCACATCAGACATGTCAGAGCTGA 243
| | | | |
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Qy      415 ATCACTGCACTGTCTGTGGGTTTCAATTAACCAATTATGGTGTACACTGGGTTGCCAG 474
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Qy      475 CCTCCAGGAAAGGCTGTGAGTGGCTGGAGTAATATGGGCTGTGGAAGCACAATTAT 534
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Qy      595 TTAAAAATGACAGAGTGTGCAAACTGATGACAAGCCATGTACTGTGCCAGTGGGGG 654
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Search completed: February 18, 2005, 23:56:50
 Job time : 151.69 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 22:26:05 ; Search time 462.528 Seconds
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Title: US-10-075-947A-2

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database :

Published Applications NA:*

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- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	714	100.0	714	8	US-08-940-544-4
2	714	100.0	714	15	US-10-075-947A-2
3	714	100.0	1173	15	US-10-075-947A-4
4	480	67.2	1479	18	US-10-682-845-60
5	480	67.2	1479	18	US-10-682-845-62
6	480	67.2	1479	18	US-10-682-845-64
7	480	67.2	1479	18	US-10-682-845-66
8	480	67.2	1479	18	US-10-682-845-68
9	480	67.2	1479	18	US-10-682-845-70
10	480	67.2	1479	18	US-10-682-845-72
11	480	67.2	1479	18	US-10-682-845-74

12	480	67.2	1479	18	US-10-682-845-76	Sequence 76, Appl
13	480	67.2	1479	18	US-10-682-845-78	Sequence 80, Appl
14	480	67.2	1479	18	US-10-682-845-80	Sequence 84, Appl
15	480	67.2	1479	18	US-10-682-845-82	Sequence 88, Appl
16	480	67.2	1479	18	US-10-682-845-84	Sequence 92, Appl
17	480	67.2	1479	18	US-10-682-845-86	Sequence 96, Appl
18	480	67.2	1479	18	US-10-682-845-88	Sequence 100, Appl
19	417	58.4	1683	15	US-10-207-655-267	Sequence 267, App
20	416	58.3	825	15	US-10-207-655-253	Sequence 253, App
21	394.8	55.3	734	9	US-09-742-693-29	Sequence 29, Appl
22	393.2	55.1	739	17	US-10-353-721-12	Sequence 12, Appl
23	383.2	53.7	1931	18	US-10-416-011-1	Sequence 1, Appl1
24	365.6	51.2	785	15	US-10-207-655-337	Sequence 337, App
25	365.6	51.2	1491	15	US-10-207-655-338	Sequence 338, App
26	365.6	51.2	1645	15	US-10-207-655-339	Sequence 339, App
27	365.6	51.2	1645	15	US-10-207-655-340	Sequence 340, App
28	364.4	51.0	825	15	US-10-207-655-356	Sequence 356, App
29	364.4	51.0	1536	15	US-10-207-655-357	Sequence 357, App
30	364.4	51.0	1696	15	US-10-207-655-358	Sequence 358, App
31	364.4	51.0	1696	17	US-10-107-991B-2	Sequence 2, Appl1
32	358	50.1	877	18	US-10-450-384-3	Sequence 3, Appl1
33	318	44.5	420	8	US-08-973-518-3	Sequence 3, Appl1
34	318	44.5	420	9	US-09-007-093-3	Sequence 3, Appl1
35	318	44.5	420	17	US-10-428-754-3	Sequence 3, Appl1
36	312.8	43.8	1056	18	US-10-333-235A-8	Sequence 8, Appl1
37	312.8	43.8	1431	18	US-10-333-235A-10	Sequence 10, Appl
38	312.8	43.8	1702	18	US-10-333-235A-11	Sequence 11, Appl
39	311.6	43.6	5011	19	US-10-844-837-101	Sequence 101, App
40	307.2	43.0	360	14	US-10-332-187-1	Sequence 1, Appl1
41	307	43.0	1407	18	US-10-429-660-9	Sequence 9, Appl1
42	307	43.0	1407	18	US-10-429-662-9	Sequence 9, Appl1
43	302.6	42.4	357	17	US-10-239-656-22	Sequence 22, Appl1
44	300.4	42.1	657	18	US-10-609-019-35	Sequence 35, Appl
45	300.4	42.1	1440	14	US-10-196-793A-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-08-940-544-4
; Sequence 4, Application US/08940544B
; Publication No. US20020018783A1
; GENERAL INFORMATION:
; APPLICANT: SABELAIN, MICHEL
; APPLICANT: CHEONG, NAI-KONG V.
; APPLICANT: KRAUSE, ANJA
; APPLICANT: GUO, HONG-FEN
; TITLE OF INVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: WSK.P-035-US
; CURRENT FILING DATE: 1997-09-30
; EARLIER APPLICATION NUMBER: PCT/US97/04427
; EARLIER FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 714
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: 3G6-bcfv
US-08-940-544-4

Query Match 100.0%; Score 714; DB 8; Length 714;
Best Local Similarity 100.0%; Pred. No. 8.8e-216; Indels 0; Gaps 0;
Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGATTGTGATGACCCAGACTCCCAATTCCTGCTTATATAGCAGAGAGAGGTTACC 60

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RESULT 2
US-10-075-947a-2
; Sequence 2, Application US/10075947A
; Publication No. US20030147808A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Fen
; APPLICANT: Rivilin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK P-013-2
; CURRENT APPLICATION NUMBER: US/10/075,947A
; PRIORITY FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/142,974
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/US97/04427
; PRIOR FILING DATE: 1997-03-20
; PRIOR FILING DATE: 1996-03-20
; PRIOR APPLICATION NUMBER: 60/013,703
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
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OTHER INFORMATION: 366-scfv
US-10-075-947a-2
Query Match 100.0%; Score 714; DB 15; Length 714;
Best Local Similarity 100.0%; Pred. No. 8.8e-216; Indels 0; Gaps 0;
Matches 714; Conservative 0; Mismatches 0;

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DB 1 AGTATTGTGATGACCCAGAGCTCCCAAAATTCCTGCTGTATACAGAGAGACAGGGTTACC 60
QY 61 ATAACTGCAAGGCGCAGTCAAGTGTGATATGATGTGGCTTGGTACCAAGAACCA 120
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QY 241 GAAGACCTGCGAGTTTATTTCTGTACAGAGATTAATAGCTCGCTCGAGAGGGGGACCAAG 300
DB 241 GAAGACCTGCGAGTTTATTTCTGTACAGAGATTAATAGCTCGCTCGAGAGGGGGACCAAG 300
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QY 361 GTGCAGGTGAAGAGTCAAGACCTGGCTGGGCGGCTTCAAGAGCCTGTCCATGACT 420
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QY 601 ATGAACAGTCTGCAAACTGATGACACAGCCATGACTGTCGCAAGTCCGCGGGGTAAAC 660
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QY 661 TACGGCTATGCTTTGGACTATCTGGGGTCAAGAACTCACTCACTCTCTCTCA 714
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RESULT 3
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; Sequence 4, Application US/10075947A
; Publication No. US20030147808A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Nai-Kong V.
; APPLICANT: Larson, Steven M.
; APPLICANT: Guo, Hong-Fen
; APPLICANT: Rivilin, Ken
; APPLICANT: Sadelain, Michel
; TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
; FILE REFERENCE: MSK P-013-2
; CURRENT APPLICATION NUMBER: US/10/075,947A
; PRIORITY FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/142,974
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; Sequence 62, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIORITY FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-62
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Query Match          67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
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QY 534 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 593
DB 534 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 593
QY 543 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 602
DB 543 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 602
QY 594 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 653
DB 594 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 653
QY 603 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 661
DB 603 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 661
QY 654 GGGTAATGACGGCTATGCTTGTGACTATGCGGGTCAAGGAACCTCACTGCTCTCTC 713
DB 654 GGGTAATGACGGCTATGCTTGTGACTATGCGGGTCAAGGAACCTCACTGCTCTCTC 713
QY 662 -----AGAACTGTGTCTTGTCTTACTGGGGCCAGGAGCAGCGGTCAACCGTCTCTC 713
DB 662 -----AGAACTGTGTCTTGTCTTACTGGGGCCAGGAGCAGCGGTCAACCGTCTCTC 713
```

```
RESULT 6
US-10-682-845-64
; Sequence 64, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIORITY FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-64
```

```
Query Match          67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;
```

```
QY 3 TATTGTGATGACCCAGACTCCCAATTCCTGCTGTATGACGACGAGAGGGTTACAT 62
DB 3 TATCCAGCTGACCCAGCTCAAAATTCATGTCCACATCGATGAGAACAGGGTCACGT 62
QY 63 AACCTGCAGGCCAGTGCAGAGTGTGACTAATGATGTGGCTTGTGACCAAGAGCCAG 122
DB 63 CACCTGCAGGCCAGTGCAGAGTGTGGTATCTAATGATGCTGGTATCAAGAACAGG 122
QY 123 GCACTCTCCGAATCTGTATATCTGTGATCCATTCGCTCACTGAGTCCCTGATCG 182
DB 123 GCATCTCTTAAAGCATGATTTACTCGGATCTTACCGGTACAGTGAAGTCCGTATCG 182
QY 183 CTTCACTGGCAGTGGATGATGAGGACGATTTCACTTACATCAGACATGTCGAGGCTGA 242
DB 183 CTTCACTGGCAGTGGATGATGAGGACGATTTCACTTACATCAGACATGTCGAGGCTGA 242
QY 243 AGACTGGCAGTTTATTTCTGTGACGAGATTATAGCT-----CGCTGGAGGGGG 293
DB 243 AGACTGGCAGAGATTTCTGTGACGAAATTAACAGCTATCCGCTCAAGTTCGCTGG 302
QY 294 GACCAAGCTGGAATTAAGTGTGAGCGGCTTACGCGGAGTGTGCTTGGCGGTGGCG 353
DB 294 GACCAAGCTGGAATTAAGTGTGAGCGGCTTACGCGGAGTGTGCTTGGCGGTGGCG 353
QY 303 GACCAAGCTGGAATTAAGTGTGAGTGTGCTTGGCGGCGGTGGCGGTGGCGGTGG 362
DB 303 GACCAAGCTGGAATTAAGTGTGAGTGTGCTTGGCGGCGGTGGCGGTGGCGGTGG 362
QY 354 ATGCAAGTGCAGGTGAGGAGTGCAGGACCTGGCTGGTGGCGCCCTCAGAGCCGTGC 413
DB 354 ATGCAAGTGCAGGTGAGGAGTGCAGGACCTGGCTGGTGGCGCCCTCAGAGCCGTGC 413
QY 414 CATCACTTGCAGTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGTTCGCA 473
DB 414 CATCACTTGCAGTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGTTCGCA 473
QY 423 CATCACTTGCAGTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGTTCGCA 482
DB 423 CATCACTTGCAGTGTCTCTGGGTTTTCATTAAACCAATTATGTGTATCACTGGTTCGCA 482
QY 474 GCTTCAGGAAAGGGCTGTGAGTGTGCTGGGAGTAAATGCGCTGTGTGAAGCACAATTA 533
DB 474 GCTTCAGGAAAGGGCTGTGAGTGTGCTGGGAGTAAATGCGCTGTGTGAAGCACAATTA 533
QY 483 GTCTCAGGAAAGGGCTGTGAGTGTGCTGGGAGTAAATGCGCTGTGTGAAGCACAATTA 542
DB 483 GTCTCAGGAAAGGGCTGTGAGTGTGCTGGGAGTAAATGCGCTGTGTGAAGCACAATTA 542
QY 534 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 593
DB 534 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 593
QY 543 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 602
DB 543 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACCAATTCCTCAAGAGCCAGTTT 602
QY 594 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 653
DB 594 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 653
QY 603 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 661
DB 603 CTTAAATATGAACAGTGTGCAATCTGATGACAGCCATGTAATCTAGTGTCCAGTGGGG 661
```

Db 483 GTCTCAGGAAAGGCTCTGGAGTGGCTGGAGTGATATGTGAGTGGTGGAAAGCACAGACTA 542

Oy	53	TAATTTGGGCTCTTAATGTCAGACTAGACAGAGCAAACTCCAAAGCCAAAGTTT	553
	543	TAATGCAAGCTTTATATCCAGACTAGACAGACAAATTCAAAGGCCAAGTTT	602
Oy	594	CTTTAAATAATGACAGCTCTGCAAACTGATGACACGCCATGTACTATCTGTGCAAGTCGGG	653
Db	603	CTTTAAATAATGACAGCTCTGCAAACTGATGACACGCCATGTACTATCTGTGCAAAATGG-	661
Oy	654	GGGTAACTACGCGCTATGCTTTGGAACTACTGCGGGGTCAAGAACTTCAGTCAACCGTCTCTC	713
Db	662	-----AGAACTGTCGCTTTGCTTACTACGGGGCCAAAGGACACAGGCTCACCGTCTCTC	713

RESULT 9

```

US-10-682-845-70
: Sequence 70. Application US/10682845
: Publication No. US20040162411A1
: GENERAL INFORMATION:
: APPLICANT: Lanzavecchia, Antonio
: TITLE OF INVENTION: Potent T cell modulating molecules
: FILE REFERENCE: G2296 US
: CURRENT APPLICATION NUMBER: US/10/682,845
: CURRENT FILING DATE: 2003-10-10
: PRIOR APPLICATION NUMBER: US 60/419,149
: PRIOR FILING DATE: 2002-10-18
: PRIOR APPLICATION NUMBER: CA 2,403,313
: PRIOR FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 89
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 70
: LENGTH: 1479
: TYPE: DNA
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: scFv EPCAMxCD3 with M10 mutant in anti-CD3 part
US-10-682-845-70

```

Query Match	67.28; Score 480; DB 18; Length 1479;
-------------	---------------------------------------

Best Local Similarity 81.5%; Pred. No. 2.1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

Oy	TATTTGATGAGCCACACCTCCGAATTCCTGCTTGATACACAGAGACAGGGTTACAT	62
Db	3 TATTCACGCTBACCCACACTCTCAAAAATTACATGTCACATCAATGAGAGACGGTCACGCT	62
Oy	63 AACCTGCAAGGCCAGTCAGAGTGTGATGATGATGCTGGCTTGATACCAACAGAGCCAGG	122
Db	63 CACCTGCAAGGCCAGTCAGATGTGGGTATCTAATGTACCTGGTATCAAGAAACCAAG	122
Oy	123 GCAGTCTCCGAAACCTGCTGATATATCTCTGCATCCCAATGGCTACACTGGAGTCCCTGATCG	182
Db	123 GCATCTCTCTAAAGCACTGATTTACTTCGGCACTCAACGGATACAGTGAATCCCTGATCG	182
Oy	183 CTTCACGTGCGAGTGATATGAGACGGAATTCCTTCACATCACTGACACTGTGACAGCTGA	242
Db	183 CTTCACAGGCGAGTGATCTGGACACAGATTTCATCTCAACATCAAGCATGTGACGTGA	242
Oy	243 AGACCTGGCAGTTTATTTCTGTGACAGGATTAAGCT-----CGCTCGAGGGGG	293
Db	243 AGACTGGCGAGATATTTCTGTGACCAATATATACAGCATCCGCTCAAGTTCCGGTGTGG	302
Oy	294 GACCAAGCTGGAATTAAGAGTGTGAGGCGGTTCAAGCGGAGAGTGGCTCTGGCGGTGGCGG	353
Db	303 GACCAAGCTCGAATPAAGAGTGTGTGTGTCTGGCGGCGAGCATCCCGTGGTGTGTGG	362
Oy	354 ATGCGAGGTGCAGGTGAAGAGTCAAGACCTTGCGTGTGGCGGCTTCAAGACCTGTCT	413
Db	363 TTCTCAGGTGAACCTGACGAGAGTCAGGACCTGTGACGCGCTTCAAGACCTGTCT	422
Oy	414 CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGAACCTGGGTTGGCCA	473
Db	423 CATCACTTGCAAGTCTGTGGTTTTCATTAACCTGATAGTGAACCTGGGTTGGCCA	482

Oy	474	GCCTCAGAAAAGGCTGCGAGTGTGGGAGTAAATAGGGCTGTGGAAAGCAAAATTA	533
Db	483	GTCCTCAGAAAAGGGCTGCGAGTGTGGGAGTAAATAGGAGTGCTGGAAAGCAAGACTA	542
Oy	534	TAATTCGGGCTTATATGTCCAGACTAGGATCAGCAAGGACAACCTCCAAGAGCCAAATTTT	593
Db	543	TAATGCAGCTTTCATATCCAGACTAGGATCAGCAAGGACAATTCCTCAAGAGCCAAATTTT	602
Oy	594	CTTAAAAATGAACAGTCTTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGCGG	653
Db	603	CTTTAAAAATGAACAGCTCTGCAAGCTAAATGACACAGCCATATATTTACTGTGCCAATAATG-	661
Oy	654	GGGTAACTAAGGCTATAGCTTTGGACTTACTGGGGGTCAAGAACTTCAGTCAACCGTCTCTC	713
Db	662	-----AGAACTGATCGTTGTGCTTACTGTGGGGCCAAAGGACACAGGTCAACCGTCTCTC	713

RESULT 10

```

US-10-682-845-72
: Sequence 72. Application US/10682845
: Publication No. US20040162111A1
: GENERAL INFORMATION:
: APPLICANT: Lanzavecchia, Antonio
: TITLE OF INVENTION: Potent T cell modulating molecules
: FILE REFERENCE: G2296 US
: CURRENT APPLICATION NUMBER: US/10/682,845
: CURRENT FILING DATE: 2003-10-10
: PRIOR APPLICATION NUMBER: US 60/419,149
: PRIOR FILING DATE: 2002-10-18
: PRIOR APPLICATION NUMBER: CA 2,403,313
: PRIOR FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 89
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 72
: LENGTH: 1479
: TYPE: DNA
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: scFv EpcAmxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-72

```

Query Match 67.2%; Score 480; DB 18; Length 1479;

Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 27

Oy	3	TATTGTGATGACCCAGACTCTCCCAATTTCTGCTGTGTATCAGACAGAGACAGGGTTACCAT	62
Db	3	TATCCAGCTGACCCAGCTCTCAAAATTCATGTCCACATCAGTATAGAGACAGGGTCAAGCT	62
Oy	63	AACCTGACAGGCGCAGTCAGAGTGTGATGATGATGTGGCTTGATACCAACGAAAGCCAGG	122
Db	63	CACCTGCMAAGGCCAGTCAGAAATGTGGGTATCTATGTAGCTCTGTGTATCAACGAAACGAG	122
Oy	123	GCAGTCTCCGAAACTGCTGATATTACTCTGCATTCACATGCTACACTGAGTCCCTGATCG	182
Db	123	GCATCTCTCCMAAGCAGCTGATTTACTTCGGCATCTCCAGGTAGACGTGAGTCCCTGATCG	182
Oy	183	CTTCACTGCGCAGTGGATATGGGACGGATTTCACTTTCAACCATGAGCACTGTGACAGGCTGA	242
Db	183	CTTTCACAGGCAATGTGATCTGGGACAGATTTCACTTCACTCAATCAGCAATGTGCACTGTGA	242
Oy	243	AGACCTGGGAGTTTATTTCTGTCAACAGAGTTATAGCT-----CGCTCGGAGGGGG	293
Db	243	AGACTTGGGAGATATTTCTGTCAACCAATATTAACAGCTATTCGCTCAAGCTTCGAGTGTGG	302
Oy	294	GACCAAGCTGGAAATATAAGGTGAGGCGGTTTCAGGCGGAGAGTGGACTCTGGCGGTGGCG	353
Db	303	GACCAAGCTCGAGATCAAAAGTGTGTGTGTCTTGGCGGCGGCGGCTTCGAGTGTGTGG	362
Oy	354	ATTCGACGTTGCAGGTGAAAGGAGTCAAGACCTTGCTGGCTGGTGGCGCCCTTCACAGAGCTGTTC	413
Db	363	TTTTCACGTTGAAATCTGCAGGAGTCAAGGACTCTGAGTGGAGCTTCACAGAGCTGTTC	422

QY 414 CATCACTTGCAGCTGTCTGTGGTTTTCATTAAACCAATTATGTGTACACTGGTTCCGCA 473
DB 423 CATCACTGCAGACAGCTCTGTGTTTCTCACTTAAGCTATGTGTACACTGGTTCCGCA 482
QY 474 GCCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATATGGCTGTGGAGACAAATTA 533
DB 483 GTCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATATGGCTGTGGAGACAAACTA 542
QY 534 TAAATCGGCTTTATGTCCAGACTGAGCATCAGAAAGCAACTCCAAAGCCAAATTT 593
DB 543 TAAATCGGCTTTATGTCCAGACTGAGCATCAGAAAGCAACTCCAAAGCCAAATTT 602
QY 594 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTAATCTGTCCAGTCGGG 653
DB 603 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTAATCTGTCCAGATGG- 661
QY 654 GGGTAAGTACGCGCTATGCTTGAAGTCTGAGGAGTCAAGAACTCAGTCAAGCTCTCTC 713
DB 662 -----AGAACTGCTGTTTGTCTTACTGAGGAGCAAGGACCAAGCTCAGCTCTCTC 713

RESULT 11
US-10-682-845-74
; Sequence 74, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzevecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 74
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAmxCD3 with M13 mutant in anti-CD3 part
US-10-682-845-74

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY 3 TATTTGATGATGACCAAGCTCCCAATTCCTGCTGTATCAGACAGAGACAGGGTTACAT 62
DB 3 TATTCACGTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGAGACAGGGTCAAGT 62
QY 63 AACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGTGGCTTGTGACCAAGAGCCAGG 122
DB 63 CACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGTGGCTTGTGACCAAGAGCCAGG 122
QY 123 GCAATCTCCGAAATGCTGATATATCTGTGATCCAAATGCTCACTGGAAGTCCCTGATG 182
DB 123 GCAATCTCTTAACACTGATATATCTGGGATCTCTACCGGTAACAGTGAAGTCCCTGATG 182
QY 183 CTTCACTGGCAGTGGATATGAGGACGATTTCACTTTCACATCAGCACTGTGACAGGCTGA 242
DB 183 CTTCACTGGCAGTGGATATGAGGACGATTTCACTTTCACATCAGCAATGTGACAGTGA 242
QY 243 AGACTGGCAGTGTATTTCTGTCTGACAGAGATTAAGCT-----CGCTCGAGAGGGG 293
DB 243 AGACTGGCAGATATTTCTGTCTGACAGATTAATTAACAGCTATCCGCTCAGCTGTGCTGG 302
QY 294 GACCAAGCTGGAATTAAGAGGTGAGCGGCTTCAAGCGAGAGTGGCTCTGCGGTGCGG 353
DB 303 GACCAAGCTGGAATTAAGAGGTGAGCGGCTTCTGCGCGCGGCTCTCGGTGCTGGTGG 362

QY 354 ATGCAAGTGCAGGTGAAGAGTCAAGACTGAGCTGAGCTGTGGCCCTTCAAGAGCTGTCTC 413
DB 363 TTCTCAGATGAAGACTGAGAGAGTCAAGACTGAGCTGTAGTCAAGCTTCAAGAGCTGTCTC 422
QY 414 CATCACTTGCAGCTGTCTGTGGTTTTCATTAAACCAATTATGTGTACACTGGTTCCGCA 473
DB 423 CATCACTGCAGACAGCTCTGTGTTTCTCACTTAAGCTATGTGTACACTGGTTCCGCA 482
QY 474 GCCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATATGGCTGTGGAGACAAATTA 533
DB 483 GTCTCCAGAAAGGGTCTGAGTGGCTGGAGTATATATGGCTGTGGAGACAAACTA 542
QY 534 TAAATCGGCTTTATGTCCAGACTGAGCATCAGAAAGCAACTCCAAAGCCAAATTT 593
DB 543 TAAATCGGCTTTATGTCCAGACTGAGCATCAGAAAGCAACTCCAAAGCCAAATTT 602
QY 594 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTAATCTGTCCAGTCGGG 653
DB 603 CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTAATCTGTCCAGATGG- 661
QY 654 GGGTAAGTACGCGCTATGCTTGAAGTCTGAGGAGTCAAGAACTCAGTCAAGCTCTCTC 713
DB 662 -----AGAACTGCTGTTTGTCTTACTGAGGAGCAAGGACCAAGCTCAGCTCTCTC 713

RESULT 12
US-10-682-845-76
; Sequence 76, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzevecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 76
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAmxCD3 with M14 mutant in anti-CD3 part
US-10-682-845-76

Query Match 67.2%; Score 480; DB 18; Length 1479;
Best Local Similarity 81.5%; Pred. No. 2,1e-141;
Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY 3 TATTTGATGATGACCAAGCTCCCAATTCCTGCTGTATCAGACAGAGACAGGGTTACAT 62
DB 3 TATTCACGTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGAGACAGGGTCAAGT 62
QY 63 AACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGTGGCTTGTGACCAAGAGCCAGG 122
DB 63 CACCTGGAAGGCCAGTCAAGTGTGAGTAATGATGTGGCTTGTGACCAAGAGCCAGG 122
QY 123 GCAATCTCCGAAATGCTGATATATCTGTGATCCAAATGCTCACTGGAAGTCCCTGATG 182
DB 123 GCAATCTCTTAAGACTGATATATCTGGGATCTCTACCGGTAACAGTGAAGTCCCTGATG 182
QY 183 CTTCACTGGCAGTGGATATGAGGACGATTTCACTTTCACATCAGCACTGTGACAGGCTGA 242
DB 183 CTTCACTGGCAGTGGATATGAGGACGATTTCACTTTCACATCAGCAATGTGACAGTGA 242
QY 243 AGACTGGCAGTGTATTTCTGTCTGACAGAGATTAAGCT-----CGCTCGAGAGGGG 293
DB 243 AGACTGGCAGATATTTCTGTCTGACAGATTAATTAACAGCTATCCGCTCAGCTGTGCTGG 302

OY	224	GACCAAGCTGGAATAATTAAGTGTGAGCCGTTACGCCGAGAGTGGTCTCTGACCGTGGCCG	353
Db	303	GACCAAGCTCGAGATCAAAAGTGTGTGTGTCTTGGCCGGCGGGCTCCCGTGTGTGTGG	362
OY	354	ATCGACAGTGCAGGTGTAAGAGTCAAGACCTGGCTGTGTGGCCGCTCAAGAGCCCTGT	413
Db	353	TTCTCAGGTGAACCTGCAGAGGTCAAGGACTGTGGCTTAAGTGCAGCCCTCAAGAGCCCTGT	422
OY	414	CATCACTTGCACCTGTCTCTGGGTTTTCAATTACCAATTATGTGTACACTGGGTTGGCA	473
Db	423	CATCACTGCAAGTCTCTGGTTTTCTATTACTACTATGTGTACACTCGGGTTGGCA	482
OY	474	GCCTCAGGAAAGGGCTGTGAGTGGCTGGGAGTAATATGGCTGTGTGAAAGCAAAATTA	533
Db	483	GTTCTCAGGAAAGGGCTGTGAGTGGCTGGGAGTAATATGGAGTGTGTGAAAGCAAGCTA	542
OY	534	TAAATTGGGCTTTATGTCCAGACTGAGCATCAGCAAGACAACCTCCAAAGGCAAGTTTT	593
Db	543	TAATCAGGTTTTCATATCAGACTGAGCATCAGCAAGACAATTCAAAGGCCAAGTTTT	602
OY	554	CTTAAAAATGAACAGCTCTGCCAACTGTATACAAGCCATGTACTACTGTGCCAGTGGGG	653
Db	603	CTTTAAAAATGAACAGCTCTGCCAAGCTATATGACACAGCCATATATTACTGTGCCAAGATGG	661
OY	654	GGGTAACCTACCGGCTATGCTTTGGACTACGTGGGTCAAGGAACCTCAGTCAACCGTCTCTC	713
Db	662	-----AGAACTGGTGTGTTTCTTACGTGGGGCCAAAGGACCAAGGTCACCGTCTCTC	713

```

RESULT 13
US-10-682-845-78
Sequence 78, Application US/10682845
Publication No. US20040162411a1
GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 1479
TYPE: DNA
ORGANISM: artificial sequence
FEATURES:
OTHER INFORMATION: scFv EPCAMxCD3 with M20 mutant in anti-CD3 part
US-10-682-845-78

```

Query Match	67.2%	Score 480;	DB 18;	Length 1479;
Best Local Similarity	81.5%;	Pred. No. 2.1e-141;		
Matches 587;	Conservative 0;	Mismatches 115;	Indels 18;	Gaps 2;

QY	3	TATGTGATGAGCCGAGACTCCCAATTCCTGTTGTATCAGAGAGACAGGGTTACCAT	62
Db	3	TATCCAGCTGAGCCCGACTCTCAAAAATTCATGTCCACATCCAGTAGGAGACAGGGTCAGCCT	62
QY	63	AACCTGCAGAAGCCAGTCCAGAGGTGAGTAATGATGTGGCTTGTAACCAACAGAGCCAGG	122
Db	63	CACCTGCAGAAGCCAGTCCAGAAATGTGGGTACTAATGTAGCTGTGTATCAACAGAAACCAAG	122
QY	123	GAAGTCTCCGAAACTGTGATATTACTGTGCATCCAACTGCTCACTGAGAGTCCCTGATCG	182
Db	123	GCAATCTCTCTAAAGCACTGATTTATCCGGCATCTCAACGGGTACAGTGGAGTCCCTGATCG	182
QY	183	CTTCACTGCGCAGTGGATATATGGGACCGGATTTCACTTTCACATCAGACATGTGCAAGCTGA	242
Db	183	CTTCCACAGGCAAGTGGATCTGGGACAGATTTCACTTCACATCAGACAAATGTGCAAGCTGA	242

QY	243	AGACCTGGGACGTTATTTCTGTGTCAGCAGGAATTAACT-----CGCTCGAAGGGG	2393
Db	243	AACTCTGGGAGGATTTCTGTGTCAGGAATATAACAATTCGCTCAAGTTCCGTGCTGG	3020
QY	294	GACCAAGCTGAAAAATAAAAGTGTGAGCGCGTTTCAGCGGAGGTGGCTCTTGCCGTGGCGG	3538
Db	303	GACCAAGCTCGAGATCAAAAGTGATGGTGTGTTCTTGCGCGCGCGCGGCTCCGGTGGTGGTG	3632
QY	354	ATGCAAGTGCAGGTGAGAGGAAGTCAAGAACCTGGCCTGGTGGCGCCTCACAGAGCTGTC	4131
Db	363	TTCCTAGGTGAAATCGCAAGAGTCAAGAACCTGGCCTGAGTGAAGCCTTCACAGAGCTGTTC	4222
QY	414	CATCACTTGACATGTCCTCGGGTTTTCAATTAACCAATTATAGGTATACATCGGGTTGGCCA	4737
Db	423	CATCACTTCGACAGTCTCTGGTTTTCTCATTAATAGCTATAGGTGTACATCGGGTTGGCCA	4822
QY	474	GCCTTCAGGAAAGGGTCTTGAGTGGCTGGGAGTAAATATGGGCTGTGGAAAGCAAAATTA	5338
Db	483	GTCTCCAGGAAAGGGTCTTGAGTGGCTGGGAGGTAAATATGGAGTGTGGAAAGCAAGACTA	5424
QY	534	TAAATTCGGCTCTTAATGTCGAGCTGAGCTGACATCGAAGGACAACTCCAAAGGCCAAGTTT	5939
Db	543	TAAATCAGCTTTCATATTCGAGCTGAGCTGACATCGAAGGACAAATTCCAAAGGCCAAGTTT	6022
QY	594	CTTAAAAATGAAACAGCTGTGCAAACTGATGACAAGCCATGTACTACTGTGCCAGTGGGG	6533
Db	603	CTTAAAAATGAAACAGCTGTGCAAGCTAATATGACAAGCCATATATTACTGTGCCAAGATGG-	6616
QY	654	GGGTATCTAAGGCTATGCTTTGGACTACTGGGGTCAAGAACTCAGTCAAGCTCTCTTC	7133
Db	662	-----AGAACTGATGTGTTTCTTATCTGGGGCCAAAGGAAACCAAGGATCAAGCTCTCTTC	7133

```

RESULT 14
US-10-682-845-80
; Sequence 80, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: artificial sequence
FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M31 mutant in anti-CD3 part
US-10-682-845-80

```

Query Match 67.2%; Score 480; DB 18; Length 1479;

Matches 587; Conservative 0; Mismatches 115; Indels 18; Gaps 2;

QY	3	TATTTGTATGATACCCAGAGATCCCAAAATTCCTGTGTATACACAGAGAGACAGGGTTACCAT	62
Db	3	TATTCAGGTGACCCAGATCTCAAAAATTCATATCCCATCAGTAGAGACAGGGTCAAGCT	62
QY	63	AACTGCAAGGCCAGTCAAGAGTGTGATGAATGATGTGGCTTGGTACCAACAGAACCCAGG	122
Db	63	CACCTGCAGAGGCCAGTCAAGATGTGGGTACTTAATGTATAGCTCGGTATCAACAGAAAACCCAGG	122
QY	123	GCAGTCTCCGAAACTGTGTATATACTGTGCATTCGATCGTACACTGAGAGTCCCTGATCG	182
Db	123	GCATATCTCTTAAGACATGATTTTACTCGGCAATCCACCGGTATCAGATGAGTCCCTGATCG	182

Oy	183	CTTCACTGGCAGTGGATATATGGGACGGAAATTCACCTTTACCAATCAGACATCTGTCAGAGCTGA	242
Db	183	CTTCACTGGCAGTGGATATATGGGACGGAAATTCACCTTTACCAATCAGACATCTGTCAGAGCTGA	242
Oy	243	AGACCTGGCAGTTTATTTCTGTCTGTCAGCAGGATATTAAGCT-----CGCTCGAGAGGGG	293
Db	243	AGACTTGGCAGAGTATTTCTGTCTGTCAGCAATATTAACAGCTATTCGGCTTCACGTTCCGGTGGCTGG	302
Oy	294	GACCAAGCTGGAAAATAAAAAGGTGGAGGCGGTTTCAGGCGGAGGTTGCTCTGGCGGTGGCGG	353
Db	303	GACCAAGCTCGAGATCAAAAGGTGGTGGTGTCTTGCGCGCGGCGGCTCCGGTGTGGTGG	362
Oy	354	ATCGCAGGTGCGAGGTGAAGAGATCGAGACCTGGCCTGGTGGGCGCCCTCAGACAGCCTGTC	413
Db	363	TTCCTCAGGTGAATCTGCAAGAGATCAGACCTGGCCTATGTCAGGCCCTCACAAGCCTGTGC	422
Oy	414	CATCACTTGCACCTGTCTCTGGGTTTTTCATTAAACCAATTATGGTGTATCACTGGGTTTCGCCA	473
Db	423	CATCACTTGCACAGCTCTCGGTTTTCTATTATACCTAGCTATGGTGTATCACTGGGTTTCGCCA	482
Oy	474	GCTTCACGAAAAGGCTCTGGAATGGCTCGGAGATATATATGGGCTGGTGGAAAGCAAAATTA	533
Db	483	GCTTCACGAAAAGGCTCTGGAATGGCTCGGAGTGTATATGGATGTGGTGGAAAGCAAGACTA	542
Oy	534	TAAATCGGCTCTTATATGTCACAGCTGAGCATCAGCAAGGACAATCCAGAGGCCAAGTTT	593
Db	543	TATATGACCTTTCAATATTCAGACTAGCATCAGCAAGGACAATTCAGAGGCCAAGTTT	602
Oy	594	CTTAAAAATGAACAGCTTGCACAACTGATGACACAGCCATGTATCTACTGTGCCAGTCCGGG	653
Db	603	CTTAAAAATGAACAGCTTGCACAGCTAATATGACACAGCCATATATTACTGTGCCAGAAATGG-	661
Oy	654	GdGTAACTAAGCGTATGCTTTGGACTACTCTGGGGTGAAGAACTCAGTCAAGCTCTCCCTC	713
Db	662	-----AGAACTGCTGCTTTGCTTACTCGGGGCCAAGGAGCACAGGTCAACGCTCTCCCTC	713
RESULT 15			
US-10-682-845-82			
Sequence 82, Application US/10682845			
Publication No. US20040162411A1			
GENERAL INFORMATION:			
APPLICANT: Lanzavecchia, Antonio			
TITLE OF INVENTION: Potent T cell modulating molecules			
FILE REFERENCE: G2296 US			
CURRENT APPLICATION NUMBER: US/10/662, 845			
CURRENT FILING DATE: 2003-10-10			
PRIOR APPLICATION NUMBER: US 60/419,149			
PRIOR FILING DATE: 2002-10-18			
PRIOR APPLICATION NUMBER: CA 2,403,313			
PRIOR FILING DATE: 2002-10-11			
NUMBER OF SEQ ID NOS: 89			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 82:			
LENGTH: 1479			
TYPE: DNA			
ORGANISM: artificial sequence			
FEATURE:			
OTHER INFORMATION: scFv EpcAMxCD3 with M58 mutant in anti-CD3 part			
US-10-682-845-82			

Query Match	67.2%;	Score 480;	DB 18;	Length 1479;
Best Local Similarly	81.5%;	Pred. No. 2.1e-141;		
Matches 567; Conservative	0;	Mismatches 115;	Indels 18;	Gaps 2;

Oy	3	TATTGTGATGACCCAGACATCCCAAAATTCCTGGTTGATCAGAGAGAGACAGGGTACCAT	62
Db	3	TATCAGACTGACCCAGATCTCAAAAATTATGTCACATGATGAGAGACAGGGTACGCT	62
Oy	63	AACTGCAAGGCCAGTCAGAGTGTGAGTATGATGATGCTTGATCCAAACAGAGGCCAGG	122
Db	63	CACCTGCAGAGGCACAGTACAAATGTGGATCTATATGATGCTGTGATTCACAGAAACAGG	122

OY	123	GCAGTCTCCGAAACGTGCGATATATACCTCTCATCTGCATTCACATCGCTACATCGAGATCCCTATCG	182
Db	123	GCAATCTCTTAAGCAGCATGATTTACTCGGCATCTCAACGGTACAGTGAATCCCTATCG	182
OY	183	CTTCACTGGCAGTGGATATATGGGACGGATTTCACTTTCAACATCAGCAGTGTGACGGCTGA	242
Db	183	CTTCAACAGGCAATGGATCTGGGACAGATTTCACTCTCAACATCAGGAATGTGACAGTCTGA	242
OY	243	AGACTTGGCAGATTATTTCTGTCTGACAGGATTAATAGCT-----CGCTCGGAGGGG	293
Db	243	AGACTTGGCAGAGTATTTCTGTCAACAATATAACAGCTATCCGCTCAGCTTCGATGCTGG	302
OY	294	GACCAAGCTGCAAAATATAAAGGTGAAGGCGGTTCAAGCGGAGGGGTCTTGGCCGGTGGCGG	353
Db	303	GACCAAGCTCGAGATCAAAAGGTGTGTGTGTCTTGGCGCGCGCGGCTCCGGTGTGTGTGG	362
OY	354	ATCGCAGGTGCAAGTGAAGGAGTCAAGACCTGGCCCTGTGTGGCGCCTCTCAACAGACCTGTC	413
Db	353	TTCTCAGGTGAACCTGCAAGGATCAAGACCTGGCTTATGTGACAGCCCTCAACAGACCTGTC	422
OY	414	CATCACTTGCACCTGTCTCTGGGTTTTCAATTAACCAATTATGTGTATCACTGGGTTGGCCA	473
Db	423	CATCACTGCACAGTCTCTGGTTTTCTCAATTAATGACTATGTGTATCACTGGGTTGGCCA	482
OY	474	GCCTCCAGGAAGGGTCTGGAATGGCTGGGAGTAATATGGCGTGGTGAAGGACCAATTAT	533
Db	483	GTCTCCAGGAAGGGTCTGGAATGGCTGGGAGTGAATATGAGTGTGAAGGACCAAGCTAT	542
OY	534	TAAATTCGGCTCTTATGTCCAGACTAGCATCAGCAAGACCAACTCCAGAGCCAAATTTT	593
Db	543	TAAATTCGGCTCTTATGTCCAGACTAGCATCAGCAAGACCAATTTCCAAAGGCCAAATTTT	602
OY	594	CTTAAAAATGAACAGCTGTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTGGGG	653
Db	603	CTTAAAAATGAACAGCTGTGCAAGCTAATATGACACAGCCATATATTACTGTGCCAGAAATGG-	661
OY	654	GGGTAACTAAGGCTATGCTTTGGACTACTGTGGGTGAAGGAACCTCAAGTACCGGCTATCTC	713
Db	662	-----AGAACTGATGTTGTTACTATGGGAGCCCAAGGAGCACCAAGGCTACCGGCTATCTC	713

Search completed: February 19, 2005, 02:16:20
Job time : 466.528 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 20:04:30 : Search time 2561.12 Seconds
(without alignments)
10611.722 Million cell updates/sec

Title: US-10-075-947A-2

Perfect score: 714

Sequence: 1 agtatgttgatgaccagac.....cctcagtcaccgtctctca 714

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312	43.7	840	4	BF690298 603309721
2	285	39.9	861	5	BUS22581 AGENCOURT
3	284	39.8	480	6	CA577562 K0711809-
4	283.4	39.7	671	2	BF182141 601804682
5	280.8	39.3	594	2	BE309592 601094848
6	276	38.7	691	2	BF578188 602094691
7	265.4	37.2	970	5	BQ940476 AGENCOURT
8	262.4	36.8	831	9	CR047446 Forward B
9	262.4	36.8	930	2	BF579344 602095631
10	259	36.3	792	7	CO567792 AGENCOURT
11	257.4	36.1	793	7	CO574382 AGENCOURT
12	253	35.4	914	7	CO558560 AGENCOURT
13	250.4	35.1	883	2	BF580610 602093730
14	250	35.0	912	5	BUS22894 AGENCOURT
15	247	34.6	664	6	BF733751 BY733751
16	245.4	34.4	831	7	CO562833 AGENCOURT
17	244.6	34.3	767	7	CO562905 AGENCOURT
18	243.6	34.1	520	2	AW917371 EST348675
19	243.4	34.1	742	7	CO567469 AGENCOURT
20	242.8	34.0	685	8	BH275985 AGENCOURT
21	242.4	33.9	899	4	BG973020 602838676
22	241.2	33.8	835	7	CO555748 AGENCOURT
23	239.6	33.6	637	2	BF531263 AGENCOURT
24	237.8	33.3	368	5	BY221929 BY221929

25	237	33.2	679	6	BY751118
26	229.4	32.1	409	6	CB805016 AMGNUT-T
27	226	31.7	359	2	BB870665
28	216.6	30.3	918	2	BF135931
29	215.6	30.2	590	8	B2168874
30	213.8	29.9	694	2	BF134274
31	212	29.7	425	2	BF578521
32	212	29.7	994	5	BUS23154
33	209.8	29.4	673	8	BH065089
34	208.2	29.2	675	7	CO202765
35	205.2	28.7	706	7	CK947954 4072740 B
36	204.2	28.6	669	7	CF108094
37	204.2	28.6	915	5	BQ949447
38	202.6	28.4	799	5	BUS22787
39	202.6	28.4	974	2	BF578595
40	202.4	28.3	985	2	BF581877
41	202	28.3	820	7	CO203049
42	202	28.3	820	7	CO203049
43	201.8	28.3	489	2	BE476735
44	201.8	28.3	765	7	CB822580
45	201.4	28.2	859	7	CO202245

ALIGNMENTS

RESULT 1
LOCUS B1690298 840 bp mRNA linear EST 18-SEP-2001
DEFINITION 603309721.F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345741 5', mRNA sequence.
ACCESSION B1690298
VERSION B1690298.1 GI:15652927
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 840)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LLM11878 row: 1 column: 06
High quality sequence stop: 828.

FEATURES

SOURCE

1. 840
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345741"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies, Inc. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 43.7%; Score 312; DB 4; Length 840;
Best Local Similarity 89.4%; Pred. No. 7.4e-80;

Matches 336; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 339 CTCTGGGGTGGCGGATCGAGTGCAGGTGGAAGAGTCAAGACTGGCTGGTGGGCC 338
Db 57 CCCAAGCTGTATCTTTTCCAGGTGAGCTGAAGCACTGGCTAGTGGGCC 116
QY 399 CTCACAGAGCTGTGCATCACTTGCACGTCTCTGGGTTTCATTAACTAATTAATGGTGT 458
Db 117 CTCACAGAGCTGTGCATCACTTGCACGTCTCTGGGTTTCATTAACTAATTAATGGTGT 176
QY 459 ACACGTGGTTCGCCAGCTCCAGGAAAGGCTCTGAGTGGCTGGAGTAATATGGCTGG 518
Db 177 AGACTGGTTCGCCAGCTCCAGGAAAGGCTCTGAGTGGCTGGAGTAATATGGCTGG 236
QY 519 TGGAGCAACAATATATATCGGCTTATGCTCAGACTGAGCATCGAAGCAACTC 578
Db 237 TGGAGCAACAATATATATCGGCTTATGCTCAGACTGAGCATCGAAGCAACTC 296
QY 579 CAAGAGCAAGTTTCTTAAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTA 638
Db 297 CAAGAGCAAGTTTCTTAAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTA 356
QY 639 CTGTGCCAGTGGGGGGGTAACTACGCGCTATGCTTGGACTGCTGGGCTAAGAACTTC 698
Db 357 CTGTGCCAGTGGGGGGGTAACTACGCGCTATGCTTGGACTGCTGGGCTAAGAACTTC 416
QY 699 AGTCACCGTCTCTCA 714
Db 417 AGTCACCGTCTCTCA 432

RESULT 2
BUS22581 861 bp mRNA linear EST 13-SEP-2002
LOCUS
DEFINITION
ABENECOURT_10154040 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6529074 5', mRNA sequence.
BUS22581
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
Plate: L1AM14128 row: j column: 18
High quality sequence stop: 723.
Location/Qualifiers
1. 861
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6529074"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1db="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 39.9%; Score 285; DB 5; Length 861;
Best Local Similarity 87.1%; Pred. No. 6,1e-72;
Matches 325; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 345 CGGTGCGGATCGCAGTGCAGTGAAGAGTCAAGACTGGCTGGCGCCCTCACA 404
Db 61 CTGTGCTGTGCTCCAGGTGAGCTGAGAGCAGGACCTGGCTGGCGCCCTCACA 120
QY 405 GAGCCGTGCATCACTTGCACGTCTCTGGGTTTCATTAACTAATTAATGGTGT 464
Db 121 GAGCCGTGCATCACTTGCACGTCTCTGGGTTTCATTAACTAATTAATGGTGT 180
QY 465 GGTTCGCCAGCTCCAGGAAAGGCTCTGAGTGGCTGGAGTAATATGGCTGG 524
Db 181 GGTTCGCCAGCTCCAGGAAAGGCTCTGAGTGGCTGGAGTAATATGGCTGG 240
QY 525 CACAAATTAATTTGGGCTTATATGTCACAGTCACTGAGCATCGAAGCAACTC 584
Db 241 CACAAATTAATTTGGGCTTATATGTCACAGTCACTGAGCATCGAAGCAACTC 300
QY 585 CCAAGTTTCTTAAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTC 644
Db 301 CCAAGTTTCTTAAATAATGAACAGTCTGCAACTGATGACACAGCCATGTACTC 360
QY 645 CAGTC---GGGGGGGTAACTACGCGCTATGCTTGGACTGCTGGGCTAAGAACTTC 701
Db 361 CAGACTCTTGTATATGATGAGCCACATGATGACTATGAGCTATGGGCTCAAGAACTCA 420
QY 702 CACCGTCTCTCA 714
Db 421 CACCGTCTCTCA 433

RESULT 3
CA577562 480 bp mRNA linear EST 19-NOV-2002
LOCUS
DEFINITION
K0711B09-5N NIA Mouse Hematopoietic Stem Cell (Jln-/C-Kit-/Sca-1-)
CDNA Library (Long) Mus musculus cDNA clone NIA:K0711B09
IMAGE:30074612 5', mRNA sequence.
CA577562
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igun.gic.nia.nih.gov
Plate: K0711 row: B column: 09
Seq primer: M13 Reverse
High quality sequence stop: 480
POLYA=No.
Location/Qualifiers
1. 480
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6Ncr"
/db_xref="niaEST:K0711B09-5N"
/db_xref="taxon:10090"
/clone="NIA:K0711B09 IMAGE:30074612"
/tissue_type="Hematopoietic Stem Cell
(Jln-/C-Kit-/Sca-1-)"
/dev_stage="Age approx. 10 weeks old"
/lab_host="DH10B"

FEATURES
source

/clone_11b="NIA Mouse Hematopoietic Stem Cell
(lin-/C-Kit-/Sca-1-) cDNA library (Long)
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (<http://19sun-gtc.nia.nih.gov/cDNA>). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Teub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer (Invitrogen):
5'-DGACTAGTCTAGATCGGAGCGCCCTTTTCTTTT-3' from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 39.8%; Score 284; DB 6; Length 480;
Best Local Similarity 86.2%; Pred. No. 1e-71;
Matches 326; Conservative 0; Mismatches 50; Indels 2; Gaps 1;

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QY 339 CTCTGGCGGTGGCGGATGCGAGTGAAGAGTCAAGACTGGCTGTGGCC 398
DB 7 CCCAAGCTGTGTCTTACCCAGTGCAGTGAAGAGTCAAGACTGGCTGTGGCC 66
QY 399 CTCACAGAGCTGTTCATCATGTGCACTGTCTGGGTTTCATTACCAATTATGGGT 458
DB 67 CTCACAGAGCTGTTCATCATGTGCACTGTCTGGGTTTCATTACCAATTATGGGT 126
QY 459 AACTGTGGGTTGCGCAGCTCCAGAGAAAGGTTCTGGAGTGGTGAATATATGGCTGG 518
DB 127 AACTGTGGGTTGCGCAGCTCCAGAGAAAGGTTCTGGAGTGGTGAATATATGGCTGG 186
QY 519 TGGAGCAGCAATTAATTTGGCTTTATGTCCAGTCAAGCATCAGCAAGACATC 578
DB 187 TGGAGCAGCAGTATATGAGCTTTTATGTCCAGTCAAGCATCAGCAAGACATC 246
QY 579 CAAGAGCAAGTTTCTTAAATAATGAACAGTCTGAACTGATGACAGCATCTACTA 638
DB 247 CAAGAGCAAGTTTCTTAAATAATGAACAGTCTGAACTGATGACAGCATCTACTA 306
QY 639 CTGTGCGCAGTGGGGG--GGTAACTACCGCTATGCTTTGACTACTGCGGGTCAAGAAC 696
DB 307 CTGTGCGCAGCAGCGGGTTACTACGTGAAGAGATGCTATGACTAGCGGGTCAAGAAC 366
QY 697 TCAGTCAACCGTCTCTCA 714
DB 367 TCAGTCAACCGTCTCTCA 384

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RESULT 4

LOCUS BF182141 671 bp mRNA linear EST 31-OCT-2000
DEFINITION 601804682P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035429 5',
mRNA sequence.

ACCESSION BF182141
VERSION BF182141.1 GI:11060283
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 671)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-romail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc. (LNL)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1AM9309 row: d column: 22
High quality sequence stop: 669.
Location/Qualifiers

FEATURES

source
1..671
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4035429"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_11b="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 39.7%; Score 283.4; DB 2; Length 671;
Best Local Similarity 84.0%; Pred. No. 1.7e-71;
Matches 320; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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QY 334 GGTGGCTTGGCGGTGGCGGATGCCAGTGAAGAGTCAAGACTGGCTGTGG 393
DB 34 GCTTCCCAAGTTTATCCCTGTGCTCCAGTGAAGAGTCAAGACTGGCTGTGG 93
QY 394 GCGGCTTCACAGAGCTGTTCATCATGTGCACTGTCTGGGTTTCATTACCAATTAT 453
DB 94 GCGGCTTCACAGAGCTGTTCATCATGTGCACTGTCTGGGTTTCATTACCAATTAT 153
QY 454 GGTGTACACTGGGTTGCGCAGCTCCAGAGAAAGGTTCTGGAGTGGTGAATATATGG 513
DB 154 GATATAACTGTGATTCGCAAAACACAGAAAGGTTCTGGAGTGGTGAATATATGG 213
QY 514 GCTGTGGAAGACAAATTAATTTGGCTTTATGTCCAGTCAAGCATCAGCAAGAC 573
DB 214 ATGGGTGAGACAAATTAATTTATTCAGCTTTCATGTCCAGTCAAGCATCAGCAAGAC 273
QY 574 AACTCAAGAGCAAGTTTCTTAAATAATGAACAGTCTGAACTGATGACAGCATCTACTA 633
DB 274 AACTCAAGAGCAAGTTTCTTAAATAATGAACAGTCTGAACTGATGACAGCATCTACTA 333
QY 634 TACTACTGTGCGCAGTGGGGGTTAACTACCGCTATGCTTTGACTACTGCGGGTCAAGAAC 693
DB 334 TACTACTGTGPAAGCGCTCAGTGTAGTCCCTATGTATGACTAGCGGGTCAAGAAC 393
QY 694 AACTCAAGTCAACCGTCTCTCA 714
DB 394 AACTCAAGTCAACCGTCTCTCA 414

```

RESULT 5

LOCUS BE309592 594 bp mRNA linear EST 26-OCT-2000
DEFINITION 601094848P1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:349635 5',
mRNA sequence.

ACCESSION BE309592
VERSION BE309592.1 GI:9168025

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 594)
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM6530 row: 0 column: 12
High quality sequence stop: 591.
Location/Qualifiers
1. 594
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489635"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt: 50mM; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

FEATURES

source

Query Match 39.3%; Score 280.8; DB 2; Length 594;
Best Local Similarity 92.3%; Pred. No. 9,4e-71;
Matches 310; Conservative 0; Mismatches 17; Indels 9; Gaps 1;

ORIGIN

1 AGTATTGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGAGAGACAGGGTTACC 60
47 AATGTTGTGATGACCCAGACTCCCAATTCCTGCTGTATCAGAGAGACAGGGTTACC 106
61 AATACTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 120
107 AATACTGCAAGGCCAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 166
121 GGGCAGTCTCCGAACTGCTGATATCTGTCATCCCAATGCTACACTGAGATCCCTGAT 180
167 GGGCAGTCTCCGAACTGCTGATATCTGTCATCCCAATGCTACACTGAGATCCCTGAT 226
181 CGCTTCACTGGCAGTGTGATGAGACGATTTTCACTTTCACCATCAGACCTGTGAGAGCT 240
227 CGCTTCACTGGCAGTGTGATGAGACGATTTTCACTTTCACCATCAGACCTGTGAGAGCT 286
241 GAAAGCTGGCAGTGTGATGAGACGATTTTCTGTCAAGAGATTTAAGCT-----CGCTCGAGGG 291
287 GAAAGCTGGCAGTGTGATGAGACGATTTTCTGTCAAGAGATTTAAGCTCGCTCGAGGG 346
292 GGAACCAAGCTGGAATTAAGTGAAGGCGGTTCA 327
347 GGAACCAAGCTGGAATTAAGTGAAGGCGGTTCA 382

RESULT 6
LOCUS BF578188
DEFINITION 602094691F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209022 5',
mRNA sequence.
ACCESSION BF578188

VERSION BF578188.1 GI:11651900
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 691)
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM9774 row: 0 column: 23
High quality sequence stop: 690.
Location/Qualifiers
1. 691
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209022"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI; Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

FEATURES

source

Query Match 38.7%; Score 276; DB 2; Length 691;
Best Local Similarity 85.6%; Pred. No. 2.5e-69;
Matches 322; Conservative 0; Mismatches 45; Indels 9; Gaps 1;

ORIGIN

339 CTCTGGCGGTGGCGGATGCGAGGTGAGTGAAGAGTCAAGACCTGGCTGGCGCC 398
54 CCCAAGCTGTGCTGCTGCTCCAGGTGACGTAAGAGTCAAGACCTGGCTGGCGCC 113
399 CTCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
114 CTCACAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 173
459 ACACGTGGTGGCGGATGCGAGGTGAGTGAAGAGTCAAGACCTGGCTGGCGCC 518
174 AAGCTGGTGGCGGATGCGAGGTGAGTGAAGAGTCAAGACCTGGCTGGCGCC 233
519 TGGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 578
234 TGGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 293
579 CAAGACCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 638
294 CAAGACCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 353
639 CTGTGCAAGTGGGCGGATGCGAGGTGAGTGAAGAGTCAAGACCTGGCTGGCGCC 698
354 CTGTGCA-----GAAATCGCACTGGGACTTTGACTTGGGGCCCAAGCAACAC 404
699 AGTCACGCTCTCTCA 714
405 TCTCACAGTCTCTCA 420

RESULT 7
LOCUS BQ940476
DEFINITION BQ940476 970 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8879458 NCI_CGAP_Co24 Mus musculus cDNA clone

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM9791 row: n column: 08
High quality sequence stop: 633.

FEATURES

source

Location/Qualifiers
1. .930
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4215751"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCL_CGAP-Co24"
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP library."

ORIGIN

Query Match 36.8%; Score 262.4; DB 2; Length 930;
Best Local Similarity 83.0%; Pred. No. 2.6e-65;
Matches 312; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 339 CTCTGCGGCTGGCGGATCCGAGTGCAGTGAGAGAGTCAAGACCTGGCTGGCGCC 398
DB 56 CCCACGCTGTCTCTCTCCAGGTGCGAGTGAGAGACAGGACCTGGCTGGCGCC 115
QY 399 CTCAGAGAGCTTCATCATCTTGCACCTGCTCTGGCTTTCATTAACCAATATAGTGT 458
DB 116 CTCACAGAGCTTCATCATCTTGCACCTGCTCTGGCTTTCATTAACCAATATAGTGT 175
QY 459 ACACTGGCTTCGCGACCTCCAGAAAGGTCTGAGTGGCTGGAGTATATGAGCTG 518
DB 176 ACATGATTCGCGAGCTCCAGGAAAGGTCTGAGTGGCTGGAGTATATGAGCTG 235
QY 519 TGGAGCACAATTAATTCGCTTATGTCACAGTACAGATACAGAGCAACTC 578
DB 236 TGGAGCACAATTAATTCGCTTATGTCACAGTACAGATACAGAGCAACTC 295
QY 579 CAAGAGCAAGTTTCTTAATAATGAACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 638
DB 296 CAAGAGCAAGTTTCTTAATAATGAACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 355
QY 639 CTGTGCGAGTGGGGGTAACTACCGCTATGCTTGGACTACTGAGGTCAGAGAACTC 698
DB 356 CTGTGCGAGTGGGGGTAACTACCGCTATGCTTGGACTACTGAGGTCAGAGAACTC 412
QY 699 AGTCACCGTCTCTCA 714
DB 413 AATCACCGTCTCTCA 428

RESULT 10
COS67792 792 bp mRNA linear EST 19-JUL-2004
LOCUS AGENCOURT 28626487 NIH_MGC_249 Rattus norvegicus cDNA clone
DEFINITION IMAGE:7379450 5', mRNA sequence.
ACCESSION COS67792
VERSION COS67792.1 GI:50380421
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 792)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM15536 row: f column: 24
High quality sequence start: 15
High quality sequence stop: 703.

FEATURES

source

Location/Qualifiers
1. .792
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7379450"
/lab_host="DH10B T0NA"
/clone_1lb="NIH_MGC_249"
/note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). CDNA
was primed using oligo-dT primer:
5'-pACTAGTCTAGATCGCAGCGCGGCC('T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary
library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

ORIGIN

Query Match 36.3%; Score 259; DB 7; Length 792;
Best Local Similarity 81.1%; Pred. No. 2.5e-64;
Matches 301; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 344 GCGGTGGCGATGCGAGTGCAGTGAAGAGTCAAGACTGGCTGTGGCGCCCTCAC 403
DB 86 GCTGTCTCTGTCGAGGTGCGAGTGAAGAGTCAAGACTGGCTGTGGCGCCCTCAC 145
QY 404 AAGCCTGTCACTTCAGTCTCTGCTGCTGCTTTCATTAACAATTAATGTTACCT 463
DB 146 AAGCCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 205
QY 464 GGGTTCGACGCTCCAGAAAGGCTGTGATGCTGTGGAATTAATGAGGCTGTGGA 523
DB 206 GGGTTCGACGCTCCAGAAAGGCTGTGATGCTGTGGAATTAATGAGGCTGTGGA 265
QY 524 GCACAATTAATTAATTCGCTTATGTCAGACTGAGTCAAGAGCAACTCCAGA 583
DB 266 ACACATTAATTAATTCAGCTTCAATCCGACTGAGCATCAGAGGACACTCCAGA 325
QY 584 GCCAAGTTTCTTAATAATGAACAGTTCGAACTGATGACACAGGCATGTACTGTG 643
DB 326 ACCAAGTTTCTTAATAATGAACAGTTCGAACTGATGACACAGGCATGTACTGTG 385
QY 644 CCAGTGGGGGGGTAACTACCGCTATGCTTGGACTACTGGGTCAAGAACTCACTG 703
DB 386 CCAGAGCACCAGGATTAAGTGTGACTTGTGATTAAGGGGCCAAGAGTCAATGTCA 445
QY 704 CCGTCTCTCA 714
DB 446 CAGTCTCTCA 456

RESULT 11

COS74382 793 bp mRNA linear EST 19-JUL-2004
LOCUS COS74382
DEFINITION AGENCOURT 28451299 NIH_MGC_248 Rattus norvegicus cDNA clone
IMAGE:736659 5', mRNA sequence.
ACCESSION COS74382
VERSION COS74382.1 GI:50387011
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 793)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contract: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bldg31.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM15503 row: b column: 01
High quality sequence start: 46
High quality sequence stop: 699.
Location/Qualifiers

FEATURES

1..793
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:736659"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_248"
/note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGTTTCTAGATCGGAGGCGGCCCT(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This is a
primary library (normalized library is NIH_MGC_249) and
was constructed by Open Biosystems. Note: this is a NIH_MGC
library"

ORIGIN

Query Match 36.1%; Score 257.4; DB 7; Length 793;
Best Local Similarity 80.9%; Pred. No. 7.3e-64;
Matches 300; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 344 GCGGTGGGATCGAGGTGAAGAGTCAAGCTGGCTGTGGCGCCCTCAG 403
DB 94 GCTGTCTCTCTCCAGGTGAGAGTCAAGCTGGCTGTGGCGCCCTCAG 153
QY 404 AGAGCTGTCTCATCTGCTCTGTGGTTTCTTAACCAATATAGTGAAC 463
DB 154 AGACCTGTCTCTCACTGCTCTGTGGTTTCTTAACCAATATAGTGAAC 213
QY 464 GGGTTCGACCTTCAGAGAAAGGTCTGAGTGGCTGGAGTAATATGGCTGGTGA 523
DB 214 GGGTTCGACCTTCAGAGAAAGGTCTGAGTGGAGTATATCTGAGTGGTGA 273
QY 524 GCACAAATTAATTCGGCTCTTATGTCAAGCTGAGATCAAGAGACACTTCAGA 583
DB 274 ACACAGATTAAATTCAGCTCAAAACCGACTGAGATCAAGAGGACACTTCAGA 333

QY 584 GCCAAGTTTCTTAAAAATGACAGTCTGCACAACTGATGACAGCCATGACTGTG 643
DB 334 GCCAAGTTTCTTAAACATGAAACGTCTGCAAACTGAAGACAGGCACTTATATGTA 393
QY 644 CCAGTCGGGGGGGTAACACTGCTTGTGACTACTGGGGTCAAGAACTCAGTCA 703
DB 394 ACAGAAATGGCCCTACTACGAGAGGTGTGTCTACTGGGGCCAAAGGCACTGTGCA 453
QY 704 CCGTCTCTCA 714
DB 454 CTGTCTCTCA 464

RESULT 12
LOCUS COS58560 914 bp mRNA linear EST 19-JUL-2004
DEFINITION AGENCOURT 28542576 NIH_MGC_248 Rattus norvegicus cDNA clone
IMAGE:7374685 5', mRNA sequence.
ACCESSION COS58560
VERSION COS58560.1 GI:50371156
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 914)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contract: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bldg31.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM15523 row: p column: 11
High quality sequence start: 23
High quality sequence stop: 708.
Location/Qualifiers

1..914
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7374685"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_248"
/note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGTTTCTAGATCGGAGGCGGCCCT(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This is a
primary library (normalized library is NIH_MGC_249) and
was constructed by Open Biosystems. Note: this is a NIH_MGC
library"

FEATURES

source

ORIGIN

Query Match 35.4%; Score 253; DB 7; Length 914;
Best Local Similarity 82.2%; Pred. No. 1.5e-62;
Matches 305; Conservative 0; Mismatches 60; Indels 6; Gaps 1;
QY 344 GCGGTGGGATCGAGGTGAAGAGTCAAGCTGGCTGTGGCGCCCTCAG 403
DB 305 GCGGTGGGATCGAGGTGAAGAGTCAAGCTGGCTGTGGCGCCCTCAG 403

Db	94	GCTGTGCTCTTCCCAAGTGTGACGTGAAGAGTCAAGACCTGGCTGGACGCTCAG	153
Qy	404	AGAGCCTGTCCATCACTTGCACCTGTCTCTGGGTTTCTATTACCAATTATGTGTACCT	463
Db	154	AGACCCTGTCCCTCAACCTGCACCTGTCTCTGGGTTTCTCACTAACCAAGCATATGTGTAACT	213
Qy	464	GGGTTTCGCACCTCCAGGAAAGGGTCTGAGTGGCTGGAGTAAATATGGGCTGGTGGAA	523
Db	214	GGGTTTCGCACCTCCAGGAAAGGGTCTGGAGTGGATGGGAACAATATGGAATGTGAA	273
Qy	524	GCACAAATTATATTCGGCTCTTATGTCTCAGACTGAGCATCAGCAAGACAACCTCAAGA	583
Db	274	GCAAGATTAATATTCACTGACTCTCAAAATCCGACTGAGCATCAGCAGGACACTTCAAGA	333
Qy	584	GCCAAATTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTG	643
Db	334	GCCAAATTTTCTTAAAAATGAACAGTCTGCAAACTGAAAGACAGCCATCTACTCTGTG	393
Qy	644	CCAATCGGGGGGTAACTACGGCTATGTTTGGACTACTGGGGTCAAGGAACCTCAGTCA	703
Db	394	CCA-----GGAAATACTACAGTGGTAACTTTGATTACTGGGGCCCAAGAGTCAATGTCA	447
Qy	704	CCGTCTCTCTCA	714
Db	448	CAGTCTCTCTCA	458

RESULT	13
LOCUS	BFS80610
DEFINITION	BFS80610 883 bp mRNA linear EST 12-DEC-2000 602093730P1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5' , mRNA sequence.
ACCESSION	BFS80610
VERSION	BFS80610.1
KEYWORDS	GI:11654322
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eumathyota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 883)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
 Plate: LLM9771 row: 1 column: 07
 High quality sequence stop:639.

FEATURES	source	Location/Qualifiers
1.	883	
		/organism="Mus musculus"
		/mol_type="mRNA"
		/strain="FVB/N"
		/db_xref="taxon:10090"
		/clone="IMAGE:4208022"
		/lab_host="DH10B (TI phage-resistant)"
		/clone_11b="NCI CGAP Co24"
		/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by life technologies. Note: this is a NCI CGAP Library."

ORIGIN			
Query Match	35.1%	Score 250.4;	DB 2; length 883;
Best Local Similarity	90.5%	Pred. No. 8.4e-62;	
Matches 304; Conservative	0;	Mismatches 21;	Indels 11; Gaps 3

Dy 1 AGATTTGTGANGACCCAGACTCCCAAATTCTGTGGTATCAGCAGAGA.CAGGGTTACC 60

Dd 72 ATTATTTTGATGACCCCACTCCCAANTTCCTCG-1GTATCAGCAGAGAACAGGGTTACC 130

Dy 61 ATTAACCTGCAAAGGCCAGTCAAGAGTGTGAATGATGTGGCTTGGTACCAACAGAACCA 120

Dd 131 ATAACCTGCAAAGGCCAGTCAAGAGTGTGAATGATGTAGC-TGGTACCAACAGAAGTCA 189

Dy 121 GGGCAGTCTCGAAGCTGCTGATTAATCTGTGCATCCAAATGGCTNACA.TGSGAATGCCGAT 180

Dd 190 GGGCAGTCTCTTAACCTGATATACTATGATCATCCAAATGCTATATCTGGAATGCCGAT 249

Dy 181 CGCTTCACTGGCAGTGGATATATNGGAGGAGATTTCACCTTCAACAATCAGAC.TGTGACAGCT 240

Dd 250 CGCTTCACTGGCAGTGGACATNGGAGCGGATTTTCACTTCAACATCAACACCTGTGACAGCT 309

Dy 241 GAAGACCTGGCAGTTTATTTCTGTCAACAGATTAATAGCT-----CGCTCGAGGG 291

Dd 310 GAAGACCTGGCAGTTTATTTCTGTCAACAGATTAATAGCTCTCTCGGACGTTTCGTGGA 369

Dy 292 GGGAACCAAGCTGGAATTAAGTGTGAGAGCGGATTCA 327

Dd 370 GGCAACCAAGCTGGAATCAAGCGGCTGATGTGCA 405

RESULT 14
 B0522894
 LOCUS
 DEFINITION
 AGAGCOURT 10159089 NCI CGAP_C024 Mus musculus cDNA clone
 IMAGE:6529489 5', mRNA sequence.
 ACCESSION
 B0522894
 VERSION
 B0522894.1 GI:22833332
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 912)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.

Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LNLN4129 row: 1 column: 01
 High quality sequence: stop: 653.

FEATURES	source	location/Qualifiers
1..912		
/organism="Mus musculus"		
/mol_type="mRNA"		
/strain="FVB/N"		
/db_xref="taxon:10090"		
/clone="IMAGE:6529489"		
/lab_host="DH10B (T1 phage-resistant)"		
/clone_id="NCI_CGAP_Co24"		
/note="Organ: colon; Vector: pCMV-SPORE; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library."		

ORIGIN	
Query Match	35.0%; Score 250; DB 5; Length 912;
Best Local Similarity	81.1%; Pred. No. 1,16-61;
Matches 305; Conservative	0; Mismatches 65; Indels 6; Gaps 1;
339	CTCTGGCGGTGGCGAGATGACAGTGCAGAGTGAAGAGATCAGAGCTGGCGTGGCGCC 398

Db 370 CTGTGCCAAAATGGGTATGAGAGGATTAAGACGAGGAGACGTACTTGTGACTACTG 429
Qy 684 GGGTCAAGGAACCTCAGTCACCGTCTCCCTCA 714
Db 430 GGGCCAAAGGACCACTCTCAAGTCTCTCA 460

Search completed: February 18, 2005, 23:51:48
Job time : 2568.12 secs